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(54) Title: *ENTEROCOCCUS FAECALIS* POLYNUCLEOTIDES AND POLYPEPTIDES

(57) Abstract

The present invention relates to novel genes from *Enterococcus faecalis* and the polypeptides they encode. Also provided are vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to diagnostic methods for detecting *Enterococcus* nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by *Enterococcus*.

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Enterococcus faecalis polynucleotides and polypeptides

Field of the Invention

The present invention relates to novel *Enterococcus faecalis* genes (*E. faecalis*)
5 nucleic acids and polypeptides. Also provided are vectors, host cells and recombinant
methods for producing the same. Further provided are diagnostic methods for
detecting *Enterococcus faecalis* using probes, primers, and antibodies to the *E. faecalis*
nucleic acids and polypeptides of the present invention. The invention further relates
to screening methods for identifying agonists and antagonists of *E. faecalis*
10 polypeptide activity and to vaccines using *E. faecalis* nucleic acids and polypeptides.

Background of the Invention

Enterococci have been recognized as being pathogenic for humans since the
turn of the century when they were first described by Thiercelin in 1988 as
15 microscopic organisms. The genus *Enterococcus* includes the species *Enterococcus*
faecalis or *E. faecalis* which is the most common pathogen in the group, accounting for
80 - 90 percent of all enterococcal infections. See Lewis et al. (1990) Eur J. Clin
Microbiol Infect Dis.9:111-117.

The incidence of enterococcal infections has increased in recent years and
20 enterococci are now the second most frequently reported nosocomial pathogens.
Enterococcal infection is of particular concern because of its resistance to antibiotics.
Recent attention has focused on enterococci not only because of their increasing role in
nosocomial infections, but also because of their remarkable and increasing resistance to
antimicrobial agents. These factors are mutually reinforcing since resistance allows
25 enterococci to survive in an environment in which antimicrobial agents are heavily
used; the hospital setting provides the antibiotics which eliminate or suppress
susceptible bacteria, thereby providing a selective advantage for resistant organisms,
and the hospital also provides the potential for dissemination of resistant enterococci
via the usual routes of hand and environmental contamination.

Antimicrobial resistance can be categorized into two general types: inherent or intrinsic property, and that which is acquired. Examples for intrinsic resistance, like other species characteristics, appear to reside on the chromosome. Acquired resistance results from either a mutation or acquisition of new DNA or acquisition of new DNA. The various inherent traits expressed by enterococci include resistance to semisynthetic penicillinase-resistant penicillins, cephalosporins, low levels of aminoglycosides, and low levels of clindamycin. Examples of acquired resistance include resistance to chloramphenicol, erythromycin, high levels of clindamycin, tetracycline, high levels of aminoglycosides, resistance to penicillin by means of penicillinase, fluoroquinolones, and vancomycin. Resistance to high levels of penicillin without penicillinase and resistance to fluoroquinolones are not known to be plasmid or transposon mediated and presumably are due to mutation(s).

Although the main reservoir for enterococci in humans is the gastrointestinal tract, the bacteria can also reside in the genitourinary tract and vagina.

E. faecalis has emerged as an important pathogen in endocarditis, bacteremia, urinary tract infections (UTIs), intraabdominal infections, soft tissue infections, and neonatal sepsis. See Lewis et al. (1990). In the 1970s and 1980s enterococci became firmly established as major nosocomial pathogens. They are now the fourth leading cause of hospital-acquired infection and the third leading cause of bacteremia in the United States. Fatality ratios for enterococcal bacteremia range from 12% to 68%, with death due to enterococcal sepsis in 50% of these cases. See T.G. Emori (1993) Clin. Microbiol. Rev. 6:428-442.

The ability of enterococci to colonize the gastrointestinal tract, plus the many intrinsic and acquired resistance traits, make these organisms, which usually seem to have relatively low intrinsic virulence, an excellent opportunity to become secondary invaders. Since nosocomial isolates of enterococci have displayed resistance to essentially every useful antimicrobial agent, it will likely become increasingly difficult to successfully treat and cure enterococcal infections.

Particularly when the various resistance genes are together in a single strain, an event almost certain to occur at some time in the future.

The etiology of diseases mediated or exacerbated by *Enterococcus faecalis*, involves the programmed expression of *E. faecalis* genes, and that characterizing these
5 genes and their patterns of expression would dramatically add to our understanding of the organism and its host interactions. Knowledge of the *E. faecalis* gene and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, treating and diagnosing diseases. Thus, there is a need to characterize the genome of *E. faecalis* and for polynucleotides of this
10 organism.

Summary of the Invention

The present invention provides for isolated *E. faecalis* polynucleotides and polypeptides shown in Table 1 and SEQ ID NO:1 through SEQ ID NO:496
15 (polynucleotide sequences having odd SEQ ID NOs and polypeptide sequences having even SEQ ID NOs). One aspect of the invention provides isolated nucleic acid molecules comprising polynucleotides having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the polypeptides shown in
20 Table 1; and (c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b). The invention further provides for fragments of the nucleic acid molecules of (a), (b) & (c) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical,
25 and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b) or (c) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b) or (c) above. Additional nucleic acid embodiments of the invention relate to isolated nucleic acid molecules comprising polynucleotides which encode the amino acid sequences of

epitope-bearing portions of a *E. faecalis* polypeptide having an amino acid sequence in (a) above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of using such vectors and host cells. The present invention further relates to the use of the vectors in the production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The invention further provides isolated *E. faecalis* polypeptides having an amino acid sequence selected from the group consisting of an amino acid sequence of any of the polypeptides described in Table 1, or fragments thereof.

The polypeptides of the present invention include polypeptides having an amino acid sequence with at least 70% identity, and more preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity to those described in Table 1, as well as polypeptides having an amino acid sequence at least 70% identical, more preferably at least 75% identical, and still more preferably 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to those shown, as well as isolated nucleic acid molecules encoding such polypeptides.

The present invention further provides one or more or multi-component vaccine comprising one or more of the *E. faecalis* polypeptides or polypeptides described in Table 1, or fragments thereof, together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the *E. faecalis* polypeptide(s) are present in an amount effective to elicit an immune response to members of the *Enterococcus* genus, or at least *E. faecalis*, in an animal. The *E. faecalis* polypeptides of the present invention may further be combined with one or more immunogens of one or more other Enterococcal or non-Enterococcal organisms to produce a multi-component vaccine intended to elicit an immunological response against members of the *Enterococcus* genus and, optionally, one or more non-Enterococcal organisms.

The vaccines of the present invention can be administered in a DNA form, e.g., "naked" DNA, wherein the DNA encodes one or more Enterococcal polypeptides

and, optionally, one or more polypeptides of an *Enterococcal* organism. The DNA encoding one or more polypeptides may be constructed such that these polypeptides are expressed as fusion proteins.

The vaccines of the present invention may also be administered as a
5 component of a genetically engineered organism or host cell. Thus, a genetically engineered organism or host cell which expresses one or more *E. faecalis* polypeptides may be administered to an animal. For example, such a genetically engineered organism or host cell may contain one or more *E. faecalis* polypeptides of the present invention intracellularly, on its cell surface, or in its periplasmic space. Further, such
10 a genetically engineered organism or host cell may secrete one or more *E. faecalis* polypeptides. The vaccines of the present invention may also be co-administered to an animal with an immune system modulator (e.g. CD86 and GM-CSF).

The invention also provides a method of inducing an immunological response in an animal to one or more members of the *Enterococcus* genus, preferably one or
15 more isolates of the *E. faecalis* species, comprising administering to the animal a vaccine as described above.

The invention further provides a method of inducing a protective immune response in an animal, sufficient to prevent, attenuate, or control an infection by members of the *Enterococcus* genus, preferably at least *E. faecalis* species,
20 comprising administering to the animal a composition comprising one or more of the polynucleotides or polypeptides described in Table 1, or fragments thereof. Further, these polypeptides, or fragments thereof, may be conjugated to another immunogen and/or administered in admixture with an adjuvant.

The invention further relates to antibodies elicited in an animal by the
25 administration of one or more *E. faecalis* polypeptides of the present invention and to methods for producing such antibodies and fragments thereof. The invention further relates to recombinant antibodies and fragments thereof and to methods for producing such antibodies and fragments thereof.

The invention also provides diagnostic methods for detecting the expression of

the polynucleotides of Table 1 by identifying the *Enterococcus* genus in an animal. One such method involves assaying for the presence of a polynucleotide encoding *E. faecalis* polypeptide in a sample from an animal. This expression may be assayed either directly (e.g., by assaying polypeptides using antibodies elicited in response to amino acid sequences described in Table 1) or indirectly (e.g., by assaying for antibodies having specificity for amino acid sequences described in Table 1). The expression of polynucleotides can also be assayed by detecting the nucleic acids of Table 1. An example of such a method involves the use of the polymerase chain reaction (PCR) to amplify and detect *Enterococcus* nucleic acid sequences.

The present invention also relates to nucleic acid probes having all or part of a nucleotide sequence described in Table 1 (e.g., SEQ. NOS) which are capable of hybridizing under stringent conditions to complementary nucleic acids. The invention further relates to a method of detecting one or more *Enterococcus* nucleic acids in a biological sample obtained from an animal, comprising: (a) hybridizing the sample with one or more *Enterococcus* polypeptides, comprising: (i) hybridizing the sample with one or more of the above-described nucleic acid probes under conditions such that hybridization occurs, and (b) detecting hybridization of one or more probes to the *Enterococcus* nucleic acid present in the biological sample.

Other uses of the polypeptides of the present invention include: *inter alia*, to detect *E. faecalis* in immunoassays, as epitopes or as molecular weight markers on SDS-PAGE gels, as molecular weight markers for molecular sieve gel filtration columns, to generate antibodies that specifically bind *E. faecalis* polypeptides of the present invention for the detection *E. faecalis* in immunoassays, to generate an immune response against *E. faecalis* and other *Enterococcus* species, and as vaccines against *E. faecalis*, other *Enterococcus* species and other bacteria genera.

Isolated nucleic acid molecules of the present invention, particularly DNA molecules, are useful as probes for gene mapping or for identifying *E. faecalis* in a biological sample, for instance, by Southern and Northern blot analysis. Polynucleotides of the present invention are also useful in detecting *E. faecalis* by

PCR using primers for a particular *E. faecalis* polynucleotide. Isolated polynucleotides of the present invention are also useful in making the polypeptides of the present invention.

5 Detailed Description

The present invention relates to recombinant *E. faecalis* nucleic acids and fragments thereof. The present invention further relates to recombinant *E. faecalis* polypeptides and fragments thereof. The invention also relates to methods for using these polypeptides to produce immunological responses and to confer immunological
10 protection to disease caused by members of the genus *Enterococcus*, at least isolates of the *E. faecalis* genus. The invention further relates to nucleic acid sequences which encode antigenic *E. faecalis* polypeptides and to methods for detecting *E. faecalis* nucleic acids and polypeptides in biological samples. The invention also relates to antibodies specific for the polypeptides and peptides of the present invention and
15 methods for detecting such antibodies produced in a host animal.

Definitions

The following definitions are provided to clarify the subject matter which the inventors consider to be the present invention.

20 As used herein, the phrase "pathogenic agent" means an agent which causes a disease state or affliction in an animal. Included within this definition, for examples, are bacteria, protozoans, fungi, viruses and metazoan parasites which either produce a disease state or render an animal infected with such an organism susceptible to a disease state (e.g., a secondary infection). Further included are species and strains of
25 the genus *Enterococcus* which produce disease states in animals.

As used herein, the term "organism" means any living biological system, including viruses, regardless of whether it is a pathogenic agent.

As used herein, the term "*Enterococcus*" means any species or strain of bacteria which is members of the genus *Enterococcus*. Such species and strains are

known to those of skill in the art, and include those that are pathogenic and those that are not.

As used herein, the phrase "one of the *E. faecalis* polypeptides of the present invention" means polypeptides of the amino acid sequence of one or more of the *E. faecalis* polypeptides described in Table 1 (even SEQ ID NOs). These polypeptides may be expressed as fusion proteins wherein the *E. faecalis* polypeptides of the present invention are fused to additional amino acid sequences which may be of Enterococcal or non-Enterococcal origin. This phrase further includes polypeptide comprising fragments of *E. faecalis* polypeptides of the present invention. Additional definitions are provided throughout the specification.

Explanation of Table 1

Table 1 below, provides information regarding genes which encode polypeptides of *E. faecalis*. The table lists the gene identifier which consists of the letters EF, which denote *E. faecalis*, followed immediately by a three digit numeric code, which arbitrarily number the *E. faecalis* genes of the present invention. A number from 1 through 4 follows the three digit number. A number 1 represents the full length open reading frame of the gene preceding the preceding three digit number. A number 2 represents the full length polypeptide encoded by the gene specified the preceding three digit number. A number 3 represents a polynucleotide fragment, of the gene represented by the preceding three digit number, used to produce an antigenic polypeptide. A number 4 represents an antigenic polypeptide fragment, of the gene represented by the preceding three digit number, used to stimulate an immune response or as a vaccine. The polynucleotide and amino acid sequences of each gene and fragment are disclosed in the Sequence Listing under the SEQ ID NO listed in Table 1.

Explanation of Table 2

Table 2 lists accession numbers for the closest matching sequences between

the polypeptides of the present invention are those available through GenBank and Derwent databases. These reference numbers are the database entry numbers commonly used by those of skill in the art who will be familiar with their denominations. The descriptions of the numbers for GenBank are available from the National Center for Biotechnology Information. Column 1 lists the gene or ORF of the present invention. Column 2 lists the accession number of a "match" gene sequence in GenBank or Derwent databases. Column 3 lists the description of the "match" gene sequence. Columns 4 and 5 are the high score and smallest sum probability, respectively, calculated by BLAST. Polypeptides of the present invention that do not share significant identity/similarity with any polypeptide sequences of GenBank and Derwent are not represented in Table 2. Polypeptides of the present invention that share significant identity/similarity with more than one of the polypeptides of GenBank and Derwent are represented more than once.

15 ***Explanation of Table 3.***

The *E. faecalis* polypeptides of the present invention may include one or more conservative amino acid substitutions from natural mutations or human manipulation as indicated in Table 3. Changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein. Residues from the following groups, as indicated in Table 3, may be substituted for one another: Aromatic, Hydrophobic, Polar, Basic, Acidic, and Small,

Explanation of Table 4

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the full-length *E. faecalis* polypeptides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power Macintosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). *E. faecalis*

polypeptide shown in Table 1 may one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 4 correspond to the amino acid sequences for each full length gene sequence shown in Table 1 and in the Sequence Listing. Polypeptides of the present invention that do not have antigenic epitopes recognized by the Jameson-Wolf algorithm are not represented in Table 2.

10 *Selection of Nucleic Acid Sequences Encoding Antigenic E. faecalis Polypeptides*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. The *E. faecalis* strain V586 was deposited 2 May 1997 at the ATCC, 10801 University Blvd, Manassas, VA 20110-2209, and given accession number 55969.

Some ORFs contained in the subset of fragments of the *E. faecalis* genome disclosed herein were derived through the use of a number of screening criteria detailed below. The ORFs are bounded at the amino terminus by a methionine or valine residue and usually at the carboxy terminus by a stop codon.

Most of the selected sequences consist of complete ORFs. The polypeptides that do not comprise a complete ORF can be determined by determining whether the corresponding polynucleotide sequence comprises a stop codon after the codon for the last amino acid residue in the polypeptide sequence. It is not always preferred to express a complete ORF in a heterologous system. It may be challenging to express and purify a highly hydrophobic protein by common laboratory methods. Some of the polypeptide vaccine candidates described herein have been modified slightly to simplify the production of recombinant protein. For example, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, have been excluded from some constructs used for expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus have also been excluded from the recombinant expression

constructs. Thus, in one embodiment, a polypeptide which represents a truncated or modified ORF may be used as an antigen.

While numerous methods are known in the art for selecting potentially immunogenic polypeptides, many of the ORFs disclosed herein were selected on the basis of screening *Enterococcus faecalis* ORFs for several aspects of potential immunogenicity. One set of selection criteria are as follows:

1. *Type I signal sequence:* An amino terminal type I signal sequence generally directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Experimental evidence obtained from studies with *Escherichia coli* suggests that the typical type I signal sequence consists of the following biochemical and physical attributes (Izard, J. W. and Kendall, D. A. *Mol. Microbiol.* 13:765-773 (1994)). The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus. In addition, the central region of the signal sequence adopts an alpha-helical conformation in a hydrophobic environment. Finally, the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

2. *Type IV signal sequence:* The type IV signal sequence is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol.* 174:7345-7351 (1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, type IV signal sequences generally contain a phenylalanine residue at the +1 site relative to the cleavage site.

3. *Lipoproteins:* Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence

for lipoprotein linkage). Nearly three-quarters of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hirohashi, S. and Watanabe, C., *J. Bioenerg. Biomembr.* 22:451-471 (1990)).

5 4. *LP₁ lipoprotein*. It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. maritimus*, *E. faecalis*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V.
10 A., *ASM News* 62:405-411 (1996)). The conserved region consists of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is -P-X-T-G-X, where X is any
15 amino acid.

An algorithm for selecting antigenic and immunogenic *Enterococcus faecalis* polypeptides including the foregoing criteria was developed. The algorithm is similar to that described in U.S. patent application #8/781,986 filed January 3, 1997, which is fully incorporated by reference herein. Use of the algorithm by the inventors to
20 select immunologically useful *Enterococcus faecalis* polypeptides resulted in the selection of a number of the disclosed ORFs. Polypeptides comprising the polypeptides identified in this group may be produced by techniques standard in the art and as further described herein.

25 *Nucleic Acid Molecules*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are

provided below, for instance. A wide variety of *Enterococcus faecalis* strains that can be used to prepare *E. faecalis* genomic DNA for cloning and for obtaining polynucleotides and polypeptides of the present invention. A wide variety of *Enterococcus faecalis* strains are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). It is recognized that minor variation in the nucleic acid and amino acid sequence may be expected from *E. faecalis* strain to strain. The present invention provides for genes, including both polynucleotides and polypeptides, of the or the present invention from all the *Enterococcus faecalis* strains.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc., Foster City, CA), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion. In case of conflict between Table 1 and either the nucleic acid sequence of the clones listed in Table 1 or the amino acid sequence of the protein expressed by the clones listed in Table 1, the clones listed in Table 1 are controlling. By "nucleotide sequence" of a nucleic acid molecule or

polynucleotide sequence may mean either a DNA or an RNA sequence. Using the information provided herein, such as the amino acid sequence in Table 1, a nucleic acid molecule of the present invention encoding the *E. faecalis* polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning DNAs using genomic DNA as starting material (e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). Illustrative of the invention, the nucleic acid molecule described in Table 1 was discovered in a DNA library derived from a *E.*

5 using genomic DNA as starting material (e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). Illustrative of the invention, the nucleic acid molecule described in Table 1 was discovered in a DNA library derived from a *E.*

10 *faecalis* genomic DNA.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, DNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding

15 strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule, is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. This includes segments of DNA comprising the *E. faecalis* polynucleotides of the present invention

20 isolated from the native chromosome. These fragments include both isolated fragments consisting only of *E. faecalis* DNA and fragments comprising heterologous sequences such as vector sequences or other foreign DNA. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant

25 DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode a *E. faecalis* polypeptides and peptide of the present invention (e.g. polypeptides of Table 1).
5 That is, all possible DNA sequences that encode the *E. faecalis* polypeptides of the present invention. This includes the genetic code and species-specific codon preferences known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the bacteria mRNA to those
10 preferred by a mammalian or other bacterial host such as *E. coli*).

The invention further provides isolated nucleic acid molecules having the nucleotide sequence shown in Table 1 or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping and for identifying *E. faecalis*
15 in a biological sample, for instance, by PCR, Southern blot, Northern blot, or other form of hybridization analysis.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1, or the *E. faecalis* nucleotide
20 sequences contained in the plasmid clones listed in Table 1, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in Table 1 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10
25 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of Table 1 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of Table 1 wherein the

contiguous fragments, together between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, or by their 5' and 3' base positions. The invention includes any fragment of a contiguous nucleotide sequence, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, segments representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Table 1 or of the *E. faecalis* nucleotide sequences of the plasmid clones listed in Table 1. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, are included in the invention. Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of *E. faecalis* polypeptides identified in Table 4.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of Table 1 or the plasmid clones listed in Table 1. Any number of fragments of nucleotide sequences in Table 1 or the plasmid clones listed in Table 1, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of a polynucleotide or a nucleic acid molecules of the invention described above, for instance, nucleotide sequences of Table 1 or the *E. faecalis* sequences of the plasmid clones listed in Table 1, by stringent hybridization

conditions" is intended to mean incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (15 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.0), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides bases, and more preferably at least about 20 nucleotides bases, still more preferably at least about 30 nucleotides bases, and even more preferably about 30-70 (e.g., 50) nucleotides bases of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above. By a portion of a polynucleotide of "at least 20 nucleotides bases in length" for example, is intended 20 or more contiguous nucleotides bases nucleotides from the nucleotide sequence of the reference polynucleotide (e.g., the nucleotide sequence as shown in Table 1). Portions of a polynucleotide which hybridizes to a nucleotide sequence in Table 1, which can be used as probes and primers, may also be precisely specified by 5' and 3' base positions or by size in nucleotide bases as described above or precisely excluded in the same manner.

The nucleic acid molecules of the present invention include those encoding the full length *E. faecalis* polypeptides of Table 1 and portions of the *E. faecalis* polypeptides of Table 1. Also included in the present invention are nucleic acids encoding the above full length sequences and further comprise additional sequences, such as those encoding an added secretory leader sequence, such as a pre-, or pro- or prepro- protein sequence. Further included in the present invention are nucleic acids encoding the above full length sequences and portions thereof and further comprise additional heterologous amino acid sequences encoded by nucleic acid sequences from a different source.

Also included in the present invention are nucleic acids encoding the above protein sequences together with additional, non-coding sequences, including for

example, but not limited to, the coding for 3' sequences. These sequences include transcribed, non-transcribed sequences that may play a role in transcription, and mRNA processing, for example, ribosome binding and stability of mRNA. Also included in the present invention are additional coding sequences which provide
5 additional functionality.

Thus, a nucleic acid sequence encoding a polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in
10 a pQE vector (QIAGEN, Inc., 3259 Livestock Avenue, Crawfordsville, IN 47931), among others, many of which are commercially available. For instance, hexa-histidine provides for convenient purification of the fusion protein. See Gentz et al. (1989) Proc. Natl. Acad. Sci. 86: 821-24. The "HIS" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin
15 protein. See Wilson et al. (1984) Cell 37: 7-12. As discussed below, other such fusion proteins include the *E. faecalis* polypeptides of the present invention fused to Fc at the N- or C-terminus.

Variant and Mutant Polynucleotides

20 The present invention further relates to variants of the nucleic acid molecules which encode portions, analogs or derivatives of a *E. faecalis* polypeptides of Table 1 and variant polypeptides thereof including portions, analogs, and derivatives of the *E. faecalis* polypeptides. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a
25 given locus on a chromosome of an organism. See, e.g., B. Lewin, Genes IV (1990). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such nucleic acid variants include those produced by nucleotide substitutions, deletions, or additions. The substitutions, deletions, or additions may involve one or

more nucleotide. The mutations may be located in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

Such polypeptide variants include those produced by amino acid substitutions, deletions or additions. The substitutions, deletions, or additions may involve one or more residues. Alterations may produce conservative or non-conservative amino acid substitutions, deletions, or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The present application is directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in Table 1. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *E. faecalis* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *E. faecalis* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses for the nucleic acid molecules of the present invention that do not encode a polypeptide having *E. faecalis* activity include, *inter alia*, isolating an *E. faecalis* gene or allelic variants thereof from a DNA library, and detecting *E. faecalis*

mRNA expression of the gene of the invention is expected of containing *E. faecalis* by Northern blot analysis.

Preferred nucleic acid molecules encoding polypeptides having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences shown in Table 1, which do, in fact, encode a polypeptide having *E. faecalis* protein activity. By "a polypeptide having *E. faecalis* protein activity" is intended a polypeptide exhibiting activity similar, but not necessarily identical, to an activity of *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, an ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly affect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Table 2.

mRNA expression samples, environmental samples, suspected of containing *E. faecalis* by Northern Blot analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Table 1, which do, in fact, encode a polypeptide having *E. faecalis* protein activity. By "a polypeptide having *E. faecalis* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Table 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *E. faecalis* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. See Brutlag et al. (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=1, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3'

truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

Vectors and Host Cell

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells comprising the recombinant vectors, and the production of *E. faecalis* polypeptides and peptides of the present invention expressed by the host cells.

5 Recombinant constructs may be introduced into host cells using well known techniques such as infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in
10 complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line
15 and then transduced into host cells.

Preferred are vectors comprising *cis*-acting control regions to the polynucleotide of interest. Appropriate *trans*-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

20 In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-,
25 episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating site at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin, or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE9, pQE10 available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH146A available from Stratagene; pEF series of vectors available from Novagen; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lacI* and *lacZ* promoters, the T3, T5 and T7 promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic

promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

5 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals (for example, Davis, *et al.*, *Basic Methods In Molecular Biology* (1986)).

10 Transcription of DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 nucleotides that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of
15 the replication origin at nucleotides 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated polypeptide into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment,
20 appropriate secretion signals may be incorporated into the expressed polypeptide, for example, the amino acid sequence KDEL. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous
25 functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the

polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL5-receptor has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See Bennett, D. et al. (1995) J. Molec. Recogn. 8:52-58 and Johanson, K. et al. (1995) J. Biol. Chem. 270 (16):9459-9471.

The *E. faecalis* polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography and high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells.

Polypeptides and Fragments

The invention further provides an isolated *E. faecalis* polypeptide having an amino acid sequence in Table 1, or a peptide or polypeptide comprising a portion of the above polypeptides.

5

Variant and Mutant Polypeptides

To improve or alter the characteristics of *E. faecalis* polypeptides of the present invention, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant
10 proteins or muteins including single or multiple amino acid substitutions, deletions, additions, or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

15

N-Terminal and C-Terminal Deletion Mutants

It is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al. J. Biol. Chem., 268:2984-2988 (1993), reported modified KGF
20 proteins that had heparin binding activity even if 3, 8, or 27 N-terminal amino acid residues were missing. Accordingly, the present invention provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1, and polynucleotides encoding such polypeptides.

25

Similarly, many examples of biologically functional C-terminal deletion muteins are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein. See, e.g., Dobeli, et al. (1988) J. Biotechnology 7:199-216. Accordingly, the present invention provides polypeptides having one or more residues from the

carboxy terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini as described below.

The present invention is further directed to polynucleotide encoding portions
5 or fragments of the amino acid sequences described herein as well as to portions or
fragments of the isolated amino acid sequences described herein. Fragments include
portions of the amino acid sequences of Table 1, are at least 5 contiguous amino acid
in length, are selected from any two integers, one of which representing a N-terminal
position. The initiation codon of the polypeptides of the present inventions position
10 1. Every combination of a N-terminal and C-terminal position that a fragment at least
5 contiguous amino acid residues in length could occupy, on any given amino acid
sequence of Table 1 is included in the invention. At least means a fragment may be 5
contiguous amino acid residues in length or any integer between 5 and the number of
residues in a full length amino acid sequence minus 1. Therefore, included in the
15 invention are contiguous fragments specified by any N-terminal and C-terminal
positions of amino acid sequence set forth in Table 1 wherein the contiguous fragment
is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified
by size, in amino acid residues, rather than by N-terminal and C-terminal positions.
20 The invention includes any fragment size, in contiguous amino acid residues, selected
from integers between 5 and the number of residues in a full length sequence minus 1.
Preferred sizes of contiguous polypeptide fragments include about 5 amino acid
residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino
acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100
25 amino acid residues, about 200 amino acid residues, about 300 amino acid residues,
and about 400 amino acid residues. The preferred sizes are, of course, meant to
exemplify, not limit, the present invention as all size fragments representing any
integer between 5 and the number of residues in a full length sequence minus 1 are
included in the invention. The present invention also provides for the exclusion of any

fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

5 The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

10 *Other Mutants*

In addition to N- and C-terminal deletion forms of the protein discussed above, it also will be recognized by one of ordinary skill in the art that some amino acid sequences of the *E. faecalis* polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated,
15 it should be remembered that there will be critical areas on the protein which determine activity.

Thus, the invention further includes variations of the *E. faecalis* polypeptides which show substantial *E. faecalis* polypeptide activity or which include regions of *E. faecalis* protein such as the protein portions discussed below. Such mutants include
20 deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided. There are two main approaches for studying the tolerance of an amino acid sequence to change. See, Bowie, J. U. *et al.* (1990), Science 247:1306-1310. The first
25 method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

These studies have revealed that proteins are surprisingly tolerant of amino

acid substitutions. The studies indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described by

5 Bowie et al. (*supra*) and the references cited therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic

10 residues Phe, Tyr.

Thus, the fragment, derivative, analog, or homolog of the polypeptide of Table 1, or that encoded by the plaimds listed in Table 1, may be: (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted

15 amino acid residue may or may not be one encoded by the genetic code; or (ii) one in which one or more of the amino acid residues includes a substituent group; or (iii) one in which the *E. faecalis* polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol); or (iv) one in which the additional amino acids are fused to the above form of

20 the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the above form of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the *E. faecalis* polypeptides of the present invention may include one or

25 more amino acid substitutions, deletions, or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 3).

Amino acids in the *E. faecalis* proteins of the present invention that are

essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis. See, e.g., Cunningham et al. (1989) Science 244:1081-1085. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then
5 tested for biological activity using assays appropriate for measuring the function of the particular protein.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but
10 also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic. See, e.g., Pinckard et al., (1967) Clin. Exp. Immunol. 2:331-340; Robbins, et al., (1987) Diabetes 36:838-845; Cleland, et al., (1993) Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377.

The polypeptides of the present invention are preferably provided in an
15 isolated form, and preferably are substantially purified. A recombinantly produced version of the *E. faecalis* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in
20 the art of protein purification.

The invention further provides for isolated *E. faecalis* polypeptides comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence shown in Table 1; (b) the amino acid sequence of a full-length *E.*
25 *faecalis* polypeptide having the complete amino acid sequence shown in Table 1 excepting the N-terminal methionine; (c) the complete amino acid sequence encoded by the plasmids listed in Table 1; and (d) the complete amino acid sequence excepting the N-terminal methionine encoded by the plasmids listed in Table 1. The polypeptides of the present invention also include polypeptides having an amino acid

sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), and (d) above.

Further polypeptides of the present invention include polypeptides which
5 have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *E. faecalis* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not
10 more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *E. faecalis* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino
15 acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid
20 alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy
25 terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences

shown in Table 1 or to the amino acid sequence encoded by the plasmids listed in Table 1 can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) *Comp. App. Biosci.* 6:237-245. In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual corrections are to be made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present invention that do not have *E. faecalis* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *E. faecalis* protein expression or as agonists and antagonists capable of enhancing or inhibiting *E. faecalis* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *E. faecalis* protein binding proteins

which are also candidate agonists and antagonists according to the present invention. See, e.g., Fields et al. (1989) Nature 340:245-246.

Epitope-Bearing Portions

5 In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *E. faecalis* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the
10 immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, e.g., Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998-4002.
15 Predicted antigenic epitopes are shown in Table 4, below. It is pointed out that Table 4 only lists amino acid residues comprising epitopes predicted to have the highest degree of antigenicity. The polypeptides not listed in Table 4 and portions of polypeptides not listed in Table 4 are not considered non-antigenic. This is because they may still be antigenic *in vivo* but merely not recognized as such by the particular
20 algorithm used. Thus, Table 4 lists the amino acid residues comprising preferred antigenic epitopes but not a complete list. Amino acid residues comprising other antigenic epitopes may be determined by algorithms similar to the Jameson-Wolf analysis or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

25 As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, e.g., Sutcliffe, et al., (1983) Science 219:660-666.

Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are
5 extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. *See*, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1
10 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind
15 specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. *See* Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to
20 different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids) can bind and displace the larger
25 peptides in immunoprecipitation assays. *See, e.g.*, Wilson, et al., (1984) *Cell* 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention

designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.*, the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate an enterococcal-specific immune response or antibodies include portions of the amino acid sequences identified in Table 1. More specifically, Table 4 discloses a list of non-limiting residues that are involved in the antigenicity of the epitope-bearing fragments of the present invention. Therefore, the present invention provides for isolated and purified antigenic epitope-bearing fragments of the polypeptides of the present invention comprising a peptide sequences of Table 4. The antigenic epitope-bearing fragments comprising a peptide sequence of Table 4 preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) of a polypeptide of the present invention. That is, included in the present invention are antigenic polypeptides between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4. Therefore, in most cases, the polypeptides of Table 4 make up only a portion of the antigenic polypeptide. All combinations of sequences between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4 are included. The antigenic epitope-bearing

fragments may be specified by either the number of contiguous amino acid residues or by specific N-terminal and C-terminal positions as described above for the polypeptide fragments of the present invention, wherein the initiation codon is residue 1. Any number of the described antigenic epitope-bearing fragments of the present invention may also be excluded from the present invention in the same manner.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA **82**:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. **82**:5131-5135 at 5134).

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. *See, e.g.,* Sutcliffe, et al., *supra*; Wilson, et al., *supra*; and Bittle, et al. (1985) J. Gen. Virol. **66**:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide

antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as

m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may
5 be coupled to carrier using a more general linking agent such as glutaraldehyde.

Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two

10 weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known
15 in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of
20 peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease
25 virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the

reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

5 Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989),
10 describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C₁-C₇-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and
15 libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is hereby incorporated herein by reference.

20 As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for chimeric proteins consisting of the
25 first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Trauncker *et al.* (1988) *Nature* 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *E. faecalis* polypeptide or

fragment thereof alone. See Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *E. faecalis* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

5

Antibodies

E. faecalis protein-specific antibodies for use in the present invention can be raised against the intact *E. faecalis* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to
10 an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')₂ and
15 other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present
20 invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *E. faecalis* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific
25 activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988);

Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')₂ fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, *E. faecalis* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *E. faecalis* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *E. faecalis* polypeptide-specific antibody can be blocked by the *E. faecalis* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *E. faecalis* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *E. faecalis* polypeptide-specific antibodies.

Antibodies and fragments thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragments of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragments discussed above, i.e., by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particularly described fragment of a polypeptide of the present

invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Enterococcus* other than *E. faecalis* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Enterococcus*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Enterococcus*, are included in the present invention.

10 *Diagnostic Assays*

The present invention further relates to methods for assaying *staphylococcal* infection in an animal by detecting the expression of genes encoding *staphylococcal* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Enterococcus*-specific antibodies, nucleic acids, or
15 proteins. Analysis of nucleic acid specific to *Enterococcus* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, e.g., Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Ereemeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing
20 differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Enterococcus* has already been made, the present invention is useful for monitoring progression or
25 regression of the disease state whereby patients exhibiting enhanced *Enterococcus* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Enterococcus*

polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Enterococcus* polypeptides or nucleic acids. Methods for obtaining biological samples such as
5 tissue are well known in the art.

The present invention is useful for detecting diseases related to *Enterococcus* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable
10 technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Enterococcus* polypeptides having sufficient homology to the nucleic acid sequences identified in Table 1 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1
15 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described
20 above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium
25 phosphate buffer. A *E. faecalis* polynucleotide sequence shown in Table 1 labeled according to any appropriate method (such as the ³²P-multiprimered DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides

in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *E. faecalis* DNA sequence of the present invention is used as a
5 template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (i.e., mRNA encoding *Enterococcus* polypeptides).

10 Levels of mRNA encoding *Enterococcus* polypeptides are assayed, for e.g., using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction
15 mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers.

Alternatively, rather than labeling the primers, a labeled dNTP can be included in the
20 PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Enterococcus* polypeptides of the present invention) are
25 quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold

Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Enterococcal species including *E. faecalis* using bio chip technology. The present invention
5 includes both high density chip arrays (>1000 oligonucleotides per cm^2) and low density chip arrays (<1000 oligonucleotides per cm^2). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. The bio
10 chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *E. faecalis* or other Enterococcal infections and to monitor the genetic
15 changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in
20 the same manner as for the fragments, i.e, by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681,
25 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *E. faecalis* or other Enterococcal species and

infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using biosensors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Enterococcus* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Enterococcus* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, e.g., with urea and neutral detergent, for the liberation of *Enterococcus* polypeptides for Western-blot or dot/slot assay. See, e.g., Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell. Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Enterococcus* polypeptide can be accomplished using an isolated *Enterococcus* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Enterococcus* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Enterococcus* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and

quantify a *Enterococcus* polypeptide. The amount of a *Enterococcus* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In
5 another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Enterococcus* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Enterococcus*
10 polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be
15 brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group,
20 which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include
25 radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Enterococcus* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include



malate dehydrogenase, Enterococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and
5 acetylcholine esterase.

Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}To , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Ci , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled monoclonal antibody by the liver. In
10 addition, this radionuclide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumor tissues, particularly the liver, and therefore enhances specificity of tumor
15 localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin
20 label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an
25 oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977)

Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

5 In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *E. faecalis* infection. Such a kit may include an isolated *E. faecalis* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*E. faecalis* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific
10 embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached.
15 Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *E. faecalis* antigen can be detected by binding of the reporter labeled antibody to the anti-*E. faecalis* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *E. faecalis* infection in a subject. This detection method includes reacting a body fluid, preferably
20 serum, from the subject with an isolated *E. faecalis* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled
25 antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or

covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

5 The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Enterococcal species including *E. faecalis* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Enterococcal species, including *E. faecalis*. Bio chip and
10 biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Enterococcal species, including *E. faecalis* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and
15 environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

 The bio chips of the present invention may further comprise polypeptide
20 sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide
25 sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *E. faecalis* or other Enterococcal infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug

development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention
5 may be specified in the same manner as for the fragments, i.e. by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Enterococcal species, including *E. faecalis*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos.
10 and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

15 ***Treatment:***

Agonists and Antagonists - Assays and Molecules

The invention also provides a method of screening compounds to identify those which enhance or block the biological activity of the *E. faecalis* polypeptides of the present invention. The present invention further provides where the compounds
20 kill or slow the growth of *E. faecalis*. The ability of *E. faecalis* antagonists, including *E. faecalis* ligands, to prophylactically or therapeutically block antibiotic resistance may be easily tested by the skilled artisan. See, e.g., Straden et al. (1997) J Bacteriol. 179(1):9-16.

An agonist is a compound which increases the natural biological function or
25 which functions in a manner similar to the polypeptides of the present invention, while antagonists decrease or eliminate such functions. Potential antagonists include small organic molecules, peptides, polypeptides, and antibodies that bind to a polypeptide of the invention and thereby inhibit or extinguish its activity.

The antagonists may be employed for instance to inhibit peptidoglycan cross

bridge formation. Antibodies against *E. faecalis* may be employed to bind to and inhibit *E. faecalis* activity to treat antibiotic resistance. Any of the above antagonists may be employed in a composition with a pharmaceutically acceptable carrier.

5 *Vaccines*

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *E. faecalis* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be
10 more effective in eliciting protective immune responses against multiple species and strains of the *Enterococcus* genus than single polypeptide vaccines.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. See, e.g., Decker et al. (1996) J. Infect. Dis. 174:S270-275. In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent
15 vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. See, e.g., Aristegui, J. et al. (1997) Vaccine 15:7-9.

The present invention in addition to single-component vaccines includes multi-component vaccines. These vaccines comprise more than one polypeptide,
20 immunogen or antigen. Thus, a multi-component vaccine would be a vaccine comprising more than one of the *E. faecalis* polypeptides of the present invention.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *E. faecalis* polypeptides described in Table 1. For example, the
25 *E. faecalis* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *E. faecalis* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing

heterologous proteins are known in the art. *See, e.g.,* Robinson, K. et al. (1997) Nature Biotech. 15:653-657; Sirard, J. et al. (1997) Infect. Immun. 65:2029-2033; Chabalgoity, J. et al. (1997) Infect. Immun. 65:2402-2412. These cells may be administered live or may be killed prior to administration. Chabalgoity, J. et al., *supra*,
5 for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *E. faecalis* polypeptides of the present invention, or
10 fragments thereof, with additional non-Enterococcal components (*e.g.,* diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Enterococcus* genus and non-Enterococcal pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA
15 vaccines are currently being developed for a number of infectious diseases. *See, et al.,* Boyer, et al. (1997) Nat. Med. 3:526-532; reviewed in Spier, R. (1996) Vaccine 14:1285-1288. Such DNA vaccines contain a nucleotide sequence encoding one or more *E. faecalis* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. For example, the direct
20 administration of plasmid DNA encoding *B. burgdorgeri* OspA has been shown to elicit protective immunity in mice against borrelial challenge. *See, Luke et al. (1997) J. Infect. Dis. 175:91-97.*

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim et al.
25 (1997) Nature Biotech. 15:641-646, for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves.

These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to Enterococcal infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a Enterococcal infection. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Enterococcus* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating Enterococcal infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *E. faecalis* polypeptides disclosed herein, or fragments thereof, as well as other *Enterococcus* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Enterococcus* cells, toxin moieties will be localized to these cells and will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a Enterococcal infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically,

the compound(s) are provided in advance of any symptoms of Enterococcal infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Enterococcus* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *E. faecalis* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

A composition is said to be "pharmacologically or physiologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will

generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *E. faecalis* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine
5 of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized
10 after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and
15 incomplete), mineral salts (for example, $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*). Other substances useful as adjuvants are the saponins
20 such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $AlK(SO_4)_2$, $AlNa(SO_4)_2$, and $AlNH_4(SO_4)$. Examples of materials suitable for use in vaccine compositions are provided in REMINGTON'S PHARMACEUTICAL SCIENCES 1324-1341 (A. Osol, ed, Mack Publishing Co, Easton, PA, (1980) (incorporated herein by reference).

25 The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharyngeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions,

suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral
5 administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening,
10 flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide). *See*, Shahin, R. et al. (1995) *Infect. Immun.* 63:1195-1200. Similarly, orally administered
15 encapsulated *Salmonella typhimurium* antigens can also be used. Allaoui-Attarki, K. et al. (1997) *Infect. Immun.* 65:853-857. Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

20 Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

25 According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in

the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000 µg/ml per dose, more
5 preferably 0.1-500 µg/ml per dose, and most preferably 10-300 µg/ml per dose.

Examples

Example 1: Isolation of a Selected DNA Clone From the Deposited Sample of E. faecalis

10 Three approaches can be used to isolate a *E. faecalis* clone comprising a polynucleotide of the present invention from any *E. faecalis* genomic DNA library. The *E. faecalis* strain V586 has been deposited as a convenient source for obtaining a *E. faecalis* strain although a wide variety of strains *E. faecalis* strains can be used which are known in the art.

15 *E. faecalis* genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the
20 mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear).
25 A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and

precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *E. faecalis* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with
5 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable
10 host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the
15 appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR
20 BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of Table 1 are synthesized and used to amplify the desired DNA by PCR using a *E. faecalis* genomic DNA prep as a template. PCR is carried out
25 under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above DNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a

Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

- 5 Finally, overlapping oligos of the DNA sequences of Table 1 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

Example 2(a): Expression and Purification Enterococcal polypeptides in E. coli

- 10 The bacterial expression vector pQE60 was used for bacterial expression of some of the polypeptide fragments used in the soft tissue and systemic infection models discussed below. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding
15 site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl
20 terminus of that polypeptide.

- The DNA sequence encoding the desired portion of a *E. faecalis* protein of the present invention was amplified from *E. faecalis* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *E. faecalis* polynucleotide shown in Table 1. Additional nucleotides
25 containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

 For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *E. faecalis* polynucleotide sequence in Table 1. One of

ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form.

The 3' primer has a sequence containing an appropriate restriction site followed by
5 nucleotides complementary to the 3' end of the polypeptide coding sequence of Table 1, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *E. faecalis* DNA fragment and the vector pQE60 were digested with restriction enzymes which recognize the sites in the primers and the digested
10 DNAs were then ligated together. The *E. faecalis* DNA was inserted into the restricted pQE60 vector in a manner which places the *E. faecalis* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture was transformed into competent *E. coli* cells using
15 standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), was used in carrying out the illustrative example described herein. This strain, which was only one of many that are suitable for expressing a *E. faecalis* polypeptide, is available commercially
20 (QIAGEN, Inc., *supra*). Transformants were identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA was isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs were grown overnight ("O/N") in
25 liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture was used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells were grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") was then added to a final concentration of 1 mM to induce transcription

from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently were incubated further for 3 to 4 hours. Cells then were harvested by centrifugation.

The cells were then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8.

5 The cell debris was removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide was loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity were purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the
10 supernatant was loaded onto the column in 6 M guanidine-HCl, pH 8, the column was first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *E. faecalis* polypeptide was eluted with 6 M guanidine-HCl, pH 5.

The purified protein was then renatured by dialyzing it against
15 phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of
20 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole was removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein was stored at 4° C or frozen at -80° C.

Some of the polypeptide of the present invention were prepared using a non-
25 denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture was resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm was

approximately 10-20 O.D. ml. The suspension was then put through three freeze thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells were lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample was then centrifuged at
5 15,000 RPM for 30 minutes at 4°C. The supernatant was passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction was collected.

The pre-cleared flow-through was applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag
10 bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant was loaded onto the column in Lysis Buffer A at 4°C, the column was first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column was washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-
15 Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein was eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations were used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM
20 Imidazole. The fractions containing the purified protein were analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein was then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein was stored at 4°C or frozen at -80°.

The following alternative method may be used to purify *E. faecalis* expressed
25 in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per

unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

5 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

10 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

 Following high speed centrifugation (30,000 x g) to remove insoluble particles, 15 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

 To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared 20 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same 25 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

 Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive

Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A₂₈₀ monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 2(b): Alternative Expression and Purification Enterococcal polypeptides in E. coli

The vector pQE10 was alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of Table 1 were amplified using PCR oligonucleotide primers from genomic *E. faecalis* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid

sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were
5 selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain
10 its reading frame with that of *E. faecalis* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences encoding the amino acid sequences of Table 1 may also be cloned and expressed as fusion proteins by a protocol similar to that described
15 directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

20

Example 2(c): Alternative Expression and Purification of Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in
25 this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *E. faecalis* amino acid sequence is amplified from an *E. faecalis* genomic DNA prep the deposited DNA

clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *E. faecalis* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

5 For cloning a *E. faecalis* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers
10 contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

 The amplified *E. faecalis* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs
15 are then ligated together. Insertion of the *E. faecalis* DNA into the restricted pQE60 vector places the *E. faecalis* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

20 The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for
25 expressing *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *E. faecalis* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. faecalis* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

The following alternative method may be used to purify *E. faecalis* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer

(Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

5 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles,
10 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared
15 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same
20 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive
25 Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5.

Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after
5 the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

10 *Example 2(d): Cloning and Expression of E. faecalis in Other Bacteria*

E. faecalis polypeptides can also be produced in: *E. faecalis* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods
15 Chang et al., U.S. Patent No. 4,952,508.

Example 3: Cloning and Expression in COS Cells

A *E. faecalis* expression plasmid is made by cloning a portion of the DNA encoding a *E. faecalis* polypeptide into the expression vector pDNAI/Amp or
20 pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several
25 codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived

from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

5 A DNA fragment encoding a *E. faecalis* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *E. faecalis* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of
10 *E. faecalis* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *E. faecalis* DNA, a stop codon, and a convenient restriction site.

 The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested
15 with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis
20 or other means for the presence of the fragment encoding the *E. faecalis* polypeptide

 For expression of a recombinant *E. faecalis* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *E. faecalis* by the vector.

25 Expression of the *E. faecalis*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM

NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression
5 product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 4: Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *E. faecalis* polypeptide in this
10 example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the
15 chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.,* Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target
20 enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one
25 or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rousc Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell

41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718.

Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the
5 expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV-I. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. faecalis* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551). For the polyadenylation of the mRNA
10 other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as *gpt*, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

15 The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphatase by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *E. faecalis* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a
20 restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *E. faecalis* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified
25 again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for

transfection. Five μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme
5 that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well
10 petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM , 2 μM , 5 μM , 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of
15 100-200 μM . Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 5: Quantitative Murine Soft Tissue Infection Model for E. faecalis

Compositions of the present invention, including polypeptides and peptides,
20 are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following quantitative murine soft tissue infection model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present
25 invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 with sterilized Cytodex 3 microcarrier beads preswollen in sterile PBS (3g/100ml). Mice are anesthetized briefly until docile, but still mobile and injected with 0.2 ml of the Cytodex 3 bead/bacterial mixture into each animal subcutaneously in the inguinal region. After four days, counting the day of injection as day one, mice are sacrificed and the contents of the abscess is excised and placed in a 15 ml conical tube containing 1.0ml of sterile PBS. The contents of the abscess is then enzymatically treated and plated as follows.

The abscess is first disrupted by vortexing with sterilized glass beads placed in the tubes. 3.0mls of prepared enzyme mixture (1.0ml Collagenase D (4.0 mg/ml), 1.0ml Trypsin (6.0 mg/ml) and 8.0 mls PBS) is then added to each tube followed by a 20 min. incubation at 37C. The solution is then centrifuged and the supernatant drawn off. 0.5 ml dH2O is then added and the tubes are vortexed and then incubated for 10 min. at room temperature. 0.5 ml media is then added and samples are serially diluted and plated onto agar plates, and grown overnight at 37C. Plates with distinct and separate colonies are then counted, compared to positive and negative control samples, and quantified. The method can be used to identify composition and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

Example 6: Murine Systemic Neutropenic Model for E. faecalis Infection

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following qualitative murine systemic neutropenic model. Mice (e.g., NIH Swiss female mice, approximately 7
5 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.
10 Mice are then injected with 250 - 300 mg/kg cyclophosphamide intraperitoneally. Counting the day of C.P. injection as day one, the mice are left untreated for 5 days to begin recovery of PMNL'S.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8
15 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 in 4% Brewer's yeast in media. Mice are injected with the bacteria/brewer's yeast challenge intraperitoneally. The Brewer's yeast solution alone is used as a control. The mice are then monitored twice daily for the first week following challenge, and once a day for the next week to
20 ascertain morbidity and mortality. Mice remaining at the end of the experiment are sacrificed. The method can be used to identify compositions and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of
25 humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific
5 embodiments described herein, which are intended as single illustrations of individual
aspects of the invention. Functionally equivalent methods and components are within
the scope of the invention, in addition to those shown and described herein and will
become apparant to those skilled in the art from the foregoing description and
accompanying drawings. Such modifications are intended to fall within the scope of
10 the appended claims.

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF001-1 (SEQ ID NO:1)

TGAAAGAATA TTGCCAGAAC GTGGCGAGCA AATTGTTTTA TAAATTTTTT TAAGGGAGAG
 AAAAAAATGA AGTTCAAAAC TCTAGCAACA ACAGTGTTAG CAACCGCAGC TATTTTCGCA
 TTGGGGGCTT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
 AAGGAAGATA CGACAATCAC TTTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
 ACAAATTAAT CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
 CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTGCA CTTTAACTTC ACCAAAAGAT
 TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
 TTAGTGGAAT TAAAACCATA TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
 ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAAATACGG CATTCCATTT
 AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTG TGAAAGAATA TGGTGTGAA
 GTACCGAAAA CATTAGAGGA ATTAAGAGAA GCTTCTAAAA CAATTACGA AAAATCCAAC
 AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGGAAATGAAA
 AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTC ACAAGAAGTC
 GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
 TATTTATCTG GCCCATTTGC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT
 GCTGGTTTTG TTCAAAAAGA TGCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
 CCTGAAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTCGATAG TGCTACGCCA
 GAACAACGGA CAGCGGCAT TGAATTCATG AAATTCCTAG CTACTCCTGA TTCACAATTG
 TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTTACA CAGTGATGAG
 TACAAAAAAT CTAAGACAAC CAAAGTACCT GCACAACTTG AAAACGCAGT AAAAGATTTA
 TTCGCTATCC CAGTAGAAGA AAATGCTGAT TCAGCCTATA ATGAAATGCG GACAATTATG
 GAAAGTATTT TTGCTTCATC AAATAAAGAC ACGAGAAAAA TATTGAAAGA TGCAACATCA
 CAATTTGAAC AAGCATGGAA CCAATAA

EF001-2 (SEQ ID NO:2)

MKFKTLATTT VLATAAIFAL GACGNGNGAK ESNDIVKEVK
 EDTTITFWHA MNGVQEEALT KLTKDFMKEN PKIKVELQNO SAYPDLQAKI NSTLTSFKDL
 PTITQAYPGW LWNAAQDEML VDLKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGIPFN
 KSTEMLFYNA DLLKEYGVEV PKTLEELKEA SKTIYEKSNK EVVGAGFDSL NNYAIGMKN
 KGVDNFNKDL LTSKDSQEVV DYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIAAG
 GFVQKDAEAG GYEVGVAPRP EKINLQQGTD IYMFDSATPE QRTAAFEFMK FLATPDSQLY
 WAQQTGYMPI LESVLHSDEY KNSKTTKVPA QLENAVKDLF AIPVEENADS AYNEMRTIME
 SIFASSNKDT RKLLKDATSQ FEQAWNQ

EF001-3 (SEQ ID NO:3)

TT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
 AAGGAAGATA CGACAATCAC TTTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
 ACAAATTAAT CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
 CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTGCA CTTTAACTTC ACCAAAAGAT
 TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
 TTAGTGGAAT TAAAACCATA TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
 ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAAATACGG CATTCCATTT
 AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTG TGAAAGAATA TGGTGTGAA
 GTACCGAAAA CATTAGAGGA ATTAAGAGAA GCTTCTAAAA CAATTACGA AAAATCCAAC
 AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGGAAATGAAA
 AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTC ACAAGAAGTC
 GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
 TATTTATCTG GCCCATTTGC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCTGTTTTT TTTCAAAAAGA TCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
 CCTSAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTGATAG TGCTACGCCA
 GAACAACGGA CAGCGGCATT TGAATTCATG AAATTCTTAG CTACTCCTGA TTCACAATTG
 TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTTACA CAGTGATGAG
 TACAAAAATT CTAAGACAAC CAAASTACCT GCACAACTT AAAACGCAST AAAAGATTTA
 TTGCTATCC CAGTAGAAGA AAATCTGAT TCAGCCTATA ATGAAATGCG GACAATTATG
 GAAATATTT TCTCTCATG AAATAAAGAC ACGAGAAAAT TATTGAAAGA TGCAACATCA
 CAATTTGAAC AAGCATGGAA CCAA

EF001-4 (SEQ ID NO:4)

CGNGNGAK ESNLIVKEVK
 EDTTITFWHA MNGVQEEALT KLTKDFMKEN PKIKVELQNC SAYPDLQAKI NSTLTSPKDL
 PTITQAYPGW LWNAAQDEML VILKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGI PFN
 KSTEMLFYNA DLLKEYGVEV PFTLEELKEA SKTIYEKSNK EVVGAGFDSL NNYIAIGMKN
 KGVFNKDLDT LTSKDSQEVV IYYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIAAG
 GFVQKDAEAG GYEYGVAPRP EKINLQCGTD IYMFDSATPE QRTAAFEFMK FLATPDSQLY
 WAQQTGYMPI LESVLHSDEY KNSKTKVPA QLENAVKDLF AIPVEENADS AYNEMRTIME
 SIFASSNKDT RKLLKDATSQ FEQAWNQ

EF002-1 (SEQ ID NO:5)

TAAATAGCGG AGGTAGTACA AATGAAATTT TGGAAAAAAG GCTTAACAGC GGCAGCGCTG
 TTAGCAGTGG CGGCAGTAAC TTTAACAGCA TGTGGTGGTT CAACTGAAAA GAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTTGGAATTA TGACACGACC
 CCAGAATTTG AGAAATTTAT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACGG ATATTTTAAC CATGAAAAAC TTACTTTTCAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTTAG ATATCGAACC TGCCAAAGCA
 ACTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTT
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTCCTTA TCCCGATAAC
 TTAAGTTGGG ATGAATATGA AGCGTTAGCG AAAAAATTAT CTAAACCAGA AGAACAAGTA
 TATGGTGCCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGGAAA CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGCC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAACA GTAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCCCT CTTATAAAAC AGATGAAATT
 GATAAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACAA AAAGCCTTTA
 ACCCAGATAC AATTAATTTA G

EF002-2 (SEQ ID NO:6)

MKFW KKGLTAAALL AVAAVTLTAC GGSSEKKATE KSEDGKTKLT VTTWNYDTTP
 EFEKLFRAFE AENPDITIEP VDIASDDYDT KVTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVDLTDHVK LLDIEPAKAS YEMYEIDGKT YQPYRTDFW VLYYNKKMFD EAGIAYPDNL
 TWDEYELAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MCKDQSQMDF GTAKSTKVTY QSQFENSKAA MMYMGSWYMG TLLTNIDDGK TNVEWGIAEI
 PQCEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KIYFARKGMP SDESHKKPLT QIQLI

EF002-3 (SEQ ID NO:7)

A TGTGGTGGTT CAAGTGAAAA GAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTTGGAATTA TGACACGACC
 CCAGAATTGT AGAAATTATT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACCG ATATTTTAAC CATGAAAAAC TTACTTTCAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTAG ATATCGAACC TGCCAAAGCA
 AGTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTC
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTGCCTA TCCCGATAAC
 TTAAGTTGGG ATGAATATGA AGCGTTAGCG AAAAATTAT CTAACCAGA AGAACAAGTA
 TATGCTGCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGAAA CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGGC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAAAACA GTAAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCCTT CTTATAAAAC AGATGAAATT
 GATAAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACA AAAGCCTTTA
 ACCCAGATAC AATTAATT

EF002-4 (SEQ ID NO:8)

C GGSSEKKATE KSEDGKTKLT VTWNYDTP
 EFEKLFRAFE AENPDITIEP VDIASDDYDT KVTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVLDLTDHVK DLDIEPAKAS YEMYEIDGKT YAQPYRTDFW VLYYNKKMFD EAGIAYPDNL
 TWDEYEALAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MQKDQSQMDF GTAKSTKVY QSQFENSkaa MMYGWSWYMG TLLTNIDDGK TNVEWGIAEI
 PQQEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID
 KIYFARKGMP SDESHKKPLT QIQLI

EF003-1 (SEQ ID NO:9)

TAGGAGGACA AAAGAATGAA GAAGTTTAT TTAGCNACAT TCGCTGTTAT TGCAACAGTT
 ATTTTAGCTG CCTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTGC AATTGGAATC TTCAAAAGAT ATCTTGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAATTAAT CATTATGGAA GTGAGCGACA ATGTTGCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCCTTCAT GGAAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTGCTGCT TTAGCAATTT TAAATGCAAA CGGCGTGATT
 AAATTAAAAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTGCTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTACTG AATTAGCTA AAGCCTATGA TGAAAAAGAC
 ATCGCTATGG TGTTCGTGTA CCCAGCCTAC TTAGAACCTG CTGGTTTAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCTAAA GCGCCAATA TTCTGCGTT TTA

EF003-2 (SEQ ID NO:10)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MKKFYLL ATPAVIATVI LAACGGNKA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 RGYKINIMEV SDNVAYNDAY QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEBRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF003-3 (SEQ ID NO:11)

CTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GSAGATTACC
 GTTGCCGTGC AATTGGAATC TTCAAAAGAT ATCTTGGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAAATTA CATTATGGAA GTGAGCGACA ATGTTGCCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCCCTTCAT G3AAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTCGTGCT TTAGCAATTT TAAATGCAA C3GCGTGATT
 AAATTAAAAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTTACTG AATTTAGCTA AAGCCTATGA T3AAAAAGAC
 ATCGCTATGG TGTTCGTGCTA CCCAGCCTAC TTAGAACCTG CTGGTTTAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCTAAA GGCGCCAATA TTCTGCGTT T

EF003-4 (SEQ ID NO:12)

CGGNKQA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 RGYKINIMEV SDNVAYNDAY QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEBRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF004-1 (SEQ ID NO:13)

TAAATCGAAA GAAGGATGAT AGAAATGAAA AAAATGATTA AATTTGCAGG CATTGCTCTT
 ATTTTTCAG CTCTTCTCTC TGCCTGTAGC AACGCAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCAGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTT TTTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACATA GCAAAATCAA CTA AAAATGA AAATATTATT
 CCGTTAGTAA AATAA

EF004-2 (SEQ ID NO:14)

MKK MIKFIAGIALI FAALLSACSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSDEKL VKIDVKNVVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDSNSGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF004-3 (SEQ ID NO:15)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CTGTAGC AACGCAAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTC TTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACCATA GCAAAATCAA CTAAAAATGA AAATATTATT
 CCGTTAGTAA AA

EF004-4 (SEQ ID NO:16)

CSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSEKL VKIDVKNNVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDSNSGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF005-1 (SEQ ID NO:17)

TAAAAAATGA AAAAACGATT GACGATTGTG GGGATGCTTT TTCTGGCCAT TTTAGTAATG
 GTTGTTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCTT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT
 GAATCCTTTT CCAATAGTGT AGCTAAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCACAG AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTTCAG CGTTGTTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTCACAAC AATTCATTAC AAAAATGGCG AATATACTTT GGATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AATAA

EF005-2 (SEQ ID NO:18)

MKKRLTIVG MLFLAILVMV GCGKNQQATT KEKETKPEEL TLYIVRHGKT MLNTTDRVQG
 WSDAVLTPEG EKVVTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDNLKTMWQ DIADDQGVSL EEFMKNMTPE SFANSVAKLD QQREESKNNW
 PAEDYATITK RLKKGDKIV ATESANSNGN NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTIHYK NGEYTLDKVN DVSYLEAGEK ESK

EF005-3 (SEQ ID NO:19)

TTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCTT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAATCCTTTG DCAATAGTGT AGCTAAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCADAB AATCAGCCAA TTCTGGGAAT GCGAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTGAG CGTTGTTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTGACAAC AATTCATTAC AAAAATGCGG AATATACTTT GSATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AA

EF005-4 (SEQ ID NO:20)

CGKNQQATT KEKETKPEEL TLYIVRHGKT MLNTTDRVQG
 WSDAVLTPEG EKVVTTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDLNKTMWQ DIADDQGVSL EEFMKNMTPF SFANSVAKLD QOREESKNNW
 PAEDYATITK RLKKGDKIV ATESANSNGN NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTHYK NGEYTLKVN DVSYLEAGEK ESK

EF006-1 (SEQ ID NO:21)

TAAACGATAA ATGGAGGGAA TAAGATGAAA AAACGTACAT TATGGTCAGT AATTACTGTA
 GCAGTAGCTG TCTTAGTTTT AGGGGCTTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTACACAGT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG GCGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 GCGTTGGAAA GTGGCGATAT CGATGCCAAC TATTTCACAC ATGTGCCGTT CTTTAATGAA
 GCGGTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAACTA TCTTAGAAGA TGCTGGTTTA
 ATCAGCTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAAT
 ACTAAAAAGT TGAATTCAA TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTAAATTAAC TCAAACTTTG CCGTGGATCA AGGATTAAAT
 CCGAAAAAG ATCCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGGAACGGCG CTATTGTTCC AGTCAATGAA
 TAA

EF006-2 (SEQ ID NO:22)

MKK RTLWSVITVA VAVLVLGACG NKKSDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVPPFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRRT ATFDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAAVLINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLKVLRSK EVQDWITKKW NGAIVPVNE

EF006-3 (SEQ ID NO:23)

TTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTACACAGT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG GCGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 GCGTTGGAAA GTGGCGATAT CGATGCCAAC TATTTCACAC ATGTGCCGTT CTTTAATGAA
 GCGGTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAACTA TCTTAGAAGA TGCTGGTTTA
 ATCAGCTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAAT
 ACTAAAAAGT TGAATTCAA TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTAAATTAAC TCAAACTTTG CCGTGGATCA AGGATTAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCGAAAAAAG ATGCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGAACGGCG CTATTGTTCC AGTCAATGAA

EF006-4 (SEQ ID NO:24)

CG NKKSDDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVPPFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRRT ATFDDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAAVLINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLVLVLRSK EVQDWITKKW NGAIVPVNE

EF008-1 (SEQ ID NO:25)

TAAACCGTGA GAAAGAAATG GAGGAATCAA CGAATGAAAA AATTTAGTTT ATTTTPTTTTA
 AACTTTTTAG CAGGGTTAAC GTTAGCTGCT TCGGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTGGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTGGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAACCTACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT
 TCCAAAGCTT ATGATTTAAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAGTGTGCGA TAAACGTAGT ATGGAACGGG TCTCAAAGA AGTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTGCGCAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACATG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAATAA

EF008-2 (SEQ ID NO:26)

MKKFSLFFLT LLAGLTLAAC GNQAAEKKEK LAIVTNSIL SDLVKNVQGD
 KIELHSIVPI GTDPHEYEPL PEDIAKASEA DILFNGLNL ETGNGWFNK LMKTAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTEDPHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTN
 AKNYTEKLSK LHEEAKAKFA DIPDDKLLV TSEGAFKYFS KAYDLNAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVDKRSM ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNNWNLTK IHDGLMSK

EF008-3 (SEQ ID NO:27)

T TCGGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTGGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTGGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAACCTACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCDAAGCCTT ATGATTATAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACGAC GATTATTGAT ACCATTAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAAGTGTGA TAAACGTAGT ATGGAACGGG TCTCAAAAGA AATGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTTGCCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAAGTG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAA

EF008-4 (SEQ ID NO:28)

C GNQAAEKKEK LAIVTTNSIL SDLVKNVQGD
 KIELHSIVPI GTPHEVEPL PEDIAKASEA DILFFNLSNL ETGNGWFPNK LMKTAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTECFHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTEN
 AKNYTEKLSK LHEEFAKFA DIPDDKLLV TSEGAFKYFS KAYDLNAAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVEKRSM ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNWNLTG 1HDGLMSK

EF009-1 (SEQ ID NO:29)

TGACAAATGA AAAAATTTAG TAAATTAATT GGACTTATTG GGGTATTAGC TTTTACGATT
 GCAGGTTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTATG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCTG TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTCT TGGCCCCGAGA AGAAGATCAA
 GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
 ATTGCAGAAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AAACATTGTTG TAAAAAATAA

EF009-2 (SEQ ID NO:30)

MEKFSKLIG LIGVLAFTIA GCASGSVKDT KTETVKLGTV GTKNDEWESV KDRLKKKNID
 LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSGNTV NAPLGIYANK
 LKIDITKIDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
 ELDATQTARA LQDVDAVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
 NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF009-3 (SEQ ID NO:31)

TTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTATG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCTG TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTCT TGGCCCCGAGA AGAAGATCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
ATTGCAGAAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AACATTTGG TAAAAAA

EF009-4 (SEQ ID NO:32)

CASGSVKDT KTETVKLGVV GTKNDEWESV KDRLKKKNID
LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSIGNTV NAPLGIYANK
LKDITKIKDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
ELDATQTARA LQVDVASVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF010-1 (SEQ ID NO:33)

TGAAAGAATA AAATTGTACA GGAGGAAATA AGGAATGAAA AAATGGCAAA AAGGATTAGC
CGTAGCTGGC GCACAGCTTT AGCTGTAGGA CTAAGCGCGT GCGGTAAATC TTCAAAAGAT
GCAGCGTCAA AAGGTGATGA TAGTACACCA ACGTTATTAA TGTATCGTGT TGGGGACAAA
CCAGATAATT ATGACCAATT AATCGATAAT GCGAATAAAA TTATCGAGAA AAAAAATTGGG
GCAAAATTAA AAATGGAATT TGTGGTTGG GCGGATTGGG ACCAAAAAAT GTCAACAATC
GTTGCTTCTG GTGAAAGCTA TGATATTTCA TTAGCACAAA ATTATGCAAC GAATGCACAA
AAAGGCGCCT ATGCTGATTT AACTGATTTA GCACCTAAAT ATGCCAAAGA AGCCTATGAT
CAATTGCCAG ATAACATAT TAAAGGAAAT ACGATTAATG GAAAACGTGA TGCCTTCCCA
ATTTTAGGTA ACTCTTACGG TCAACAAGTT TTAACTTTTA ATAAAGAATA TGTCGATAAA
TACAATTTAG ATATTAGTAA AGTCGATGGT AGTTATGAAA GTGCAACGGA AGTTCTAAAA
GAATTCNTA AAAANGANCC AAATATTGCT GCTTTTGCTA TCGGCCAAAC ATTCTTTGCA
ACAGGTAATT ATGACTTCCC TATTGGTAAC CAATATCCAT TTGCAGTAAA AACAACTGAT
ACTGGCTCAC CAAAAATTAT TAACCAATAT GCCGACAAAG ACATGATTAA TAACTTAAAA
GTCTTGATC AATGGTATAA AGATGGCTTG ATTCCAACAG ATGCTGCTAC AAGTACAACA
CCATATGACT TAAATACCAA TACTTGGTTT ATGCGTCAAG AAACACAAGG ACCTATGGAT
TATGGTGATA CAATCTTAAC ACAAGCTGCT GGCAAACCAC TTGTTTCTCG TCCACTAACA
GAACCATTA AAACAACAGC TCAAGCGCAA ATGGCTAACT ATGTGTTGTC AAACACGTCT
AAAAACAAAG AAAAATCTGT TGAATTGTTA GGTTTATTAA ACAGCAATCC AGAATTGTTA
AACGGACTTG TTTATGCTGA AGAAGGCAAA CAATATGAAA AAGTTGGCGA TGATCGTGTG
AAATTGTTGA AAGATTACAC ACCAACAACT CATTTGAGTG CTTGGAACAC AGGAAAACAC
TTAATCATT GGCCAGAAGA ATCTGTCCT GAAGAAATGG TTAAAGAACG TGATAAGAGC
ATCGAAGAAG CAAAAGATTC ACCAATTCTT GGTTTTACTT TTGTAAATGA TAAAGTGAAA
ACTGAAATCA CTAACGTTGC TACAGTTATG AACC GTTACG CAGCAAGCTT AAATACAGGA
ACTGTTGATC CAGAAGAAAC ACTTCCAAAA TTAATGGATG ACCTAAAAAC AGCTGGCTGG
GATAAAGTTC AAAAAGAAAT GCAAACACAA TTAGACGAAT ATATCCAATC TCAAAAATAA

EF010-2 (SEQ ID NO:34)

MAKRISR SWRTALAVGL SACGKSSKDA ASKGDDSTPT LLMYRVGDKP
DNYDQLIDNA NKIIEKKIGA KLKMEFVGWG DWDQKMSTIV ASGESYDISL AQNYATNAQK
GAYADLTDLA PKYAKEAYDQ LPDNYIKGNT INGKLYAFPI LGNSYGQQVL TFNKEYVDKY
NLDISKVDGS YESATEVLKE FXKXPNIAA FAIGQTFAT GNYDFPIGNQ YPFAVKTDT
GSPKIINQYA DKDMINNLKV LHQWYKDGLI PTDAATSTTP YDLNNTWFM RQETQGPMDY
GDTILTQAAG KPLVSRPLTE PLKTTAQAQM ANYVVANTSK NKEKSVELLG LLNSNPELLN
GLVYGEEGKQ YEKVGDDRK LKDYTPPTH LSAWNTGNNL IIWPEESVTE EMVKERDKSI
EEAKDSPILG FTFVNDKVK EITNVATVMN RYAASLNTGT VDPEETLPKL MDDLKTAGWD
KVQKEMQTQL DEYIQSQK

EF010-3 (SEQ ID NO:35)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GT GCGGTAAATC TTCAAAAGAT
 GCAGGCTCAA AAGGTGATGA TAGTACACCA AGGTTATTAA TGTATCGTGT TGGGGACAAA
 CCABATAATT ATGACCAATT AATCGATAAT GCGAATAAAA TTATCGAGAA AAAAATTGGG
 GCAAAAATTAA AAATGGAATT TGTGTTGGG GCGATTGGG ACCAAAAAAT GTCAACAATC
 GTGCTTCTG GTGAAAGCTA TGATATTTCA TTAGCACAAA ATTATGCAAC GAATGCACAA
 AAAGGCGCCT ATGCTGATTT AACTGATTTA GCAGCTAAAT ATGCCAAAGA AGCCTATGAT
 CAATTGCCAG ATAACATATAT TAAAGGAAAT AGGATTAATG GAAACTGTGA TGCCTTCCCA
 ATTTTAGGTA ACTGTTACGG TCAACAAGTT TTAACTTTAA ATAAAGAATA TGTCGATAAA
 TACAAATTAAG ATATTAGTAA AGTCGATGGT AATTATGAAA GTGCAACGGA AGTTCTAAAA
 GAATTCNTA AAAANGANCC AAATATTGCT GCTTTTGCTA TCGGCCAAAC ATTCTTTGCA
 ACAGGTAATT ATGACTTCCC TATTGGTAAC CAATATCCAT TTGCAGTAAA AACAACGTAT
 ACTGGCTCAC CAAAAATTAT TAACCAATAT GCGACAAAAG ACATGATTAA TAACTTAAAA
 GTCTTGCATC AATGCTATTA AGATGCTTG ATTGCAACAG ATGCTGCTAC AAGTACAACA
 CCATATGACT TAAATACCAA TACTTGGTTT ATGCTGCAAG AAACACAAGG ACCTATGGAT
 TATGCTGATA CAATCTTAAC ACAAGCTGCT GCGAAACCCAC TTGTTTCTCG TCCACTAACA
 GAACCATTA AACAACAGC TCAAGCGCAA ATGCTAACT ATGTTGTTGC AAACACGTCT
 AAAAACAAG AAAAATCTGT TGAATTGTTA GGTTTATTAA ACAGCAATCC AGAATTGTTA
 AACGGACTTG TTATGCTGA AGAAGGCAAA CAATATGAAA AAGTTGGCGA TGATCGTGTG
 AAATTGTTGA AAGATTACAC ACCAACAACCT CATTTGAGTG CTTGGAACAC AGGAAACAAC
 TTAATCATTG GCGCAGAAGA ATCTGCTACT GAAGAAATG TTAAGAACG TGATAAGAGC
 ATCGAAGAAG CAAAAGATTG ACCAATTCTT GGTTTTACTT TTGTAAATGA TAAAGTAAAA
 ACTGAAATCA CTAACGTTGC TACAGTTATG AACCGTTACG CAGCAAGCTT AAATACAGGA
 ACTGTTGATC CAGAAGAAAC ACTTCCAAAA TTAATGGATG ACCTAAAAAC AGCTGGCTGG
 GATAAAGTTC AAAAAGAAAT GCAACACAA TTAGACGAAT ATATCCAATC TCAAAAA

EF010-4 (SEQ ID NO:36)

CGKSSKDA ASKGDDSTPT LLMYRVGDKF
 DNYDQLIDNA NKIEKKIGA KLKMEFVGWG DWDQKMSTIV ASGESYDISL AQNYATNAQK
 GAYADLTDLA PKYAKEAYDQ LPDNYIKGNT INGKLYAFPI LGNSYGGQVL TFNKEYVDKY
 NLDISKVDGS YESATEVLKE FXKXPNIAA FAIGQTFPAT GNYDFPIGNQ YPFAVKTTDT
 GSPKIINQYA DKDMINNLKV LHQWYKDGLI PTDAATSTTP YDLNNTWTFM RQETQGPMDY
 GDTILTQAAG KPLVSRPLTE PLKTTAQAQM ANYVVANTSK NKEKSVELLG LLNSNPELLN
 GLVYGEEGKQ YEKVGDDRVK LLKDYTPPTH LSAWNTGNL IWPPEESVTE EMVKERDKSI
 EEAKDSPILG FTFVNDKVKI EITNVATVMN RYAASLNTGT VDPEETLPKL MDDLKTAGWD
 KVQKEMQTQL DEYIQSQK

EF011-1 (SEQ ID NO:37)

TAACGTTTTT GGAGGAAAAG AATGAAAAG AAATTTTTAG CAATGATGGC AGTTTCAATG
 ATGGGACTGT TAATGTTAAG TGCTTGTCAG ACAATAAAA AAACAGCAGA TTCTGCAACA
 ACAGAAACAA CAGCTAAAAC GGAAGTCACA GTCAAAGACA CCAATGGTCA ATTAACCGTT
 CCCAAAAATC CTAAGAAAGT CGTTGTTTTT GATAATGGTT CCTTGGATAC AATGGATGCA
 CTAGGTGTCG GTGACCGCGT GGTAGGTGCG CCAACTAAAA ATATCCCTGC GTATTTGAAA
 AAATACCAAA AAGTTGAATC AGCAGGCGGC ATTAAAGAAC CAGATTTAGA AAAATCAAT
 CAACTAAAAC CAGACTTAAT TATTATTCTT GGTGCTCAAC AAGATTATCA AGAACAATTA
 AAAGCCATTG CGCCAACCAT TTACTTAGCT GTAGATGCCA AAAATCCTTG GGCATCAACG
 AAACAAAATA TCGAAACGTT AGGCACTATT TTTGATAAAG AAGAGGTAGC TAAAGAAAAA
 ATAAGTGGCT TAGAAAAAGA AATTGCTGAC GTGAAAAAAC AAGCAGAAGC TAGCGCGAAT
 AATGCGCTTG TTGTGTTAGT TAACGAAGGA CAACCTTCCG CTTACGGAAA AGGCTCTCGT
 TTCGGTTTTAA TTCATGATAC ATTGCGCTTC AAAGCAGCAG ACGATAAGAT TGAAGCTTCC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACTCATGGGC AAAGTGTTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AGTAA

EF011-2 (SEQ ID NO:38)

MKKK FLAMMAVSM GLLMLSACQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPKKVVVFD NSLDTMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKEKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEYV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF011-3 (SEQ ID NO:39)

TTGTCAA ACAAATAAAA AAACAGCAGA TTCTGCAACA
 ACAGAAACAA CAGCTAAAAC GGAAGTCACA GTCAAAGACA CCAATGGTCA ATTAACCGTT
 CCCCCAAATC CTAAGAAAGT CGTTGTTTTT GATAATGGTT CCTTGGATAC AATGGATGCA
 CTAGGTGTGG GTGACCGCGT GGTAGGTGCG CCAACTAAAA ATATCCCTGC GTATTTGAAA
 AAATACCAAA AAGTTGAATC AGCAGGCGGC ATTAAAGAAC CAGATTTAGA AAAAATCAAT
 CAACTAAAA CAGACTTAAT TATTATTTCT GGTGTCACAA AAGATTATCA AGAACAATTA
 AAAGCCATTG CGCCAACCAT TTACTTAGCT GTAGATGCCA AAAATCCTTG GGCATCAACG
 AAACAAAATA TCGAAACGTT AGGCACTATT TTTGATAAAG AAGAGGTAGC TAAAGAAAAA
 ATAAGTGGCT TAGAAAAAGA AATTGCTGAC GTGAAAAAAC AAGCAGAAGC TAGCGCGAAT
 AATGCGCTTG TTGTGTTAGT TAACGAAGGA CAACTTTCCG CTTACGGAAA AGGCTCTCGT
 TTCGGTTTAA TTCATGATAC ATTTGGCTTC AAAGCAGCAG ACGATAAGAT TGAAGCTTCC
 ACTCATGGGC AAAGTGTTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AG

EF011-4 (SEQ ID NO:40)

CQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPKKVVVFD NSLDTMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKEKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEYV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF012-1 (SEQ ID NO:41)

TGAGGGGGCA ACAACATGAA ATTGGGGAAA AAAGTAGTAG GTTTGATTGC AACAGGGTTT
 CTTTGTAGCCG CATGTGGCGG AACCAGAGAA GCGGCAGAGA AAGTAGATTG GGGAAATTTA
 GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
 CAAACAACAG AAAAAATAC CTTTACAATG GCACAACATT TATTGAAGG CCTTTATCGG
 TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT

90

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGGCGCAAGT ACCACTTTAC CTTGGGGGAG GGGATTAAST GGAGCAACGG CGAGCCAATC
ACGGCCCAAG ATTTTGTGTTA TTCTTGGAAA AAAGTGGTGA CACDAGCGAC GATTGGACCG
AATGCCTATT TACTAGACAG TGTAAAAAAT AGTTTGTGAAA TACGCAACGG TGAAAAGTCA
GTGGATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAAAACAG
GGCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
TTTGTGCAAG CGCAAGGCAA AGATTACGCG TTGGATAGTG AACATTTACT TTATAGCGGG
CGATTTACGG TAGCCAATTG GATGCGGACT TCAGATACTT CGACATTGAA AAAAAATCCA
GAATACTATG ATGCGGATCA AGTGAAGTGA GAAGAAGTTG CGGTTAGCAC AATCAAAGAA
GATAATACTG GGATTAACCT ATATCAAGTG AATGAAGTAG ACTTAGTTGG CATTAACGGA
CAATATGTTT AACAATATCA AGATGATCCA GGCATGTGCA GTCATCCAGA TGTGGCCAAC
TACTTCTTAG ATTTCAACAA AAAAGAAGGA AGGCCATTAG CGAATGTGCA TTTACGAAAA
GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
TTCCGAGCTT ACASTGGCGA ATATTTGAAA AATGACGTCA AAAAAGCTCA AGGTGAATGG
ACCAAGGCCC AAGCGGATGT CGSTAAAAAA GTGAACTTTT CATTGCTGGC GGCAGACACA
GATCAAGGAA AAGCAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
TACAAAGAAG CGGAAGACAT CTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
AGTGCCCTCA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
GATTATTTCC ACTTGCGCAA TGCTATTATA ACAGAATGA

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EF012-2 (SEQ ID NO:42)

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MKLGKK VVGLIATGFL LAACGGTKEA AEKVDSGNLA AEQKISISSP APISTLDTTQ
TTDKNTFTMA QHLEGLYRF EDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
QPSFLAVVSI AWLAPQNKF VEAQKDYAL DSEHLLYSGP FTLANWDATS DTWTLKKNP
YYEADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQQYQDDPG YVSHPDVANY
FLDFNKKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
RAYSGEYLKN DVKKAQAEWT KAQADVGGKV KLSLLAADTD QGKRIAEYVQ SQLQENLPGL
EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDYFN LYAGESSYNY GNYHNAKYDQ
LVEEARTINA NNPEKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
YFHLRNAYLT E

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EF012-3 (SEQ ID NO:43)

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ATGTGGCGG AACCAAAGAA GCGGCAGAGA AAGTAGATTC GGGAAATTTA
GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
CAAACAACAG AAAAAATAC CTTTACAATG GCACAACATT TATTTGAAGG CCTTTATCGG
TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT
GGGCGCAAGT ACCACTTTAC CTTGCGGGAG GGGATTAAST GGAGCAACGG CGAGCCAATC
ACGGCCCAAG ATTTTGTGTTA TTCTTGGAAA AAAGTGGTGA CACCAGCGAC GATTGGACCG
AATGCCTATT TACTAGACAG TGTAAAAAAT AGTTTGTGAAA TACGCAACGG TGAAAAGTCA
GTGGATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAAAACAG
GCCCCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
TTTGTGCAAG CGCAAGGCAA AGATTACGCC TTGGATAGTG AACATTTACT TTATAGCGGG
CCATTTACGC TAGCCAATTG GGATGCGACT TCAGATACTT GGACATTGAA AAAAAATCCA
GAATACTATG ATGCGGATCA AGTGAAGTGA GAAGAAGTTG CGGTTAGCAC AATCAAAGAA
GATAATACTG GGATTAACCT ATATCAAGTG AATGAAGTAG ACTTAGTTGG CATTAACGGA
CAATATGTTT AACAATATCA AGATGATCCA GGCTATGTCA GTCATCCAGA TGTGGCCAAC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACTTCTTAG ATTTCAACAA AAAAGAAGGA ACGCCATTAG CGAATGTTCA TTTACGAAAA
 GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
 AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
 TTCCGAGCTT ACAGTGGCGA ATATTTGAAA AATGACGTCA AAAAAGCTCA AGCTGAATGG
 ACGAAAGCCC AAGCGGATGT CGGTAAAAAA GTGAAACTTT CATTGCTGGC GGCAGACACA
 GATCAAGGAA AACGAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
 TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
 AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
 AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
 CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
 TACAAAGAAG CGGAAGACAT CTGTGTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
 AGTGCCTCAA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
 GATTATTTCC ACTTGCGCAA TGCCTATTTA ACAGAA

EF012-4 (SEQ ID NO:44)

CGGTKEA AEKVDSGNLA AEQKISSSP APISTLDTTQ
 TTDKNTFTMA QHLFEGLYRF DDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
 AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
 QPSFLAVVSI AWLAPQNQKF VEAQGKDYL DSEHLLYSGP FTLANWDATS DTWTLKKNPE
 YYDADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQYQDDPG YVSHPDVANY
 FLDNFNKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
 RAYSGEYLKN DVKKAQAEWT KAQADVGGKV KLSLLAADTD QGKRIAERYVQ SQLQENLPGL
 EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDSEYFN LYAGESSYNY GNYHNAKYDQ
 LVEEARTINA NNEPKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
 YFHLRNAYLT E

EF013-1 (SEQ ID NO:45)

TAACGAAAAA TGAAAAAAT TGCTTTGTTC AGTATGTTAA CGTTCAGTGT ATTGTCTTTA
 AGTCTAGCAG GATGTGGAAA CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCTG
 TCTGTACCGG GTCAAAATTC TAATGTGACA GGGGAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACGAATGAA GTCCCTCAAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTCAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACGGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGGAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCGAA TGCAACTATT TTAGTGTCAC GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGGAATTTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTAGTTGTTT
 GATTTACCAA ATTAA

EF013-2 (SEQ ID NO:46)

MKKIALFS MLTFSVLSLS LAGCGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVTG ENPSENATQP SAGTDETEV PQNQAPDTNI TITNVVFNPE RNEINGTTLP
 NATITATVVG DASAQAGVFI ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEAAALFSNI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLVPG
 TKNRLDVTLN GEIGTPYLFD LPN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF013-3 (SEQ ID NO:47)

ATGTGGAAA CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCCG
 TCTGTACCGG GTCAAAATTC TAATGTGACA GGSBAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACBAATGAA GTCCCTCAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTTAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACBGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGSAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCAGG TGCAACTATT TTASTGTCAO GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGAATTTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTAATTGTTT
 GATTTACCAA AT

EF013-4 (SEQ ID NO:48)

CGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVFG ENPSENATQP SAGTDETNV PQNQAPDTNI TITNVVFNP RNEINGTTLP
 NATITATVVG DASAQGVFY ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEAALSFNSI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLVPG
 TKNRLDVTLN GEIGTPYLFDP LPN

EF014-1 (SEQ ID NO:49)

TGATGGTGGA GACTTTTTTAA GAGAGAGGAA GTACAGCCAA TGAGTAGGAA GCGAAAAATC
 AGCTTAATTA GTTTAGTCAT CATTTTGGTT TTTGTACAG TCGGCTCAGC ATACTTTGCT
 GTAGCGGGTA GCTATTTTAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
 TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
 ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
 AAGACGAAGA AAATAACCTA TTTAAGTTTG CCACGGGATA GTTTTGTTC AATTGATGCG
 AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
 TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAC
 TTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
 GCGTTTGATG GTGTCACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAACAG
 CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTGAAA GACATAGCGA TAACGATATT
 ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
 CAATCAATCA TGAAAATAAT GGACATTATT GATTCGTTAA ATGGAAACAT TCAAACATGAT
 GTGGATTCCA ATGAATTGAC TCATTTAGTC AAAGAAGGTT TGACTTGGAC CAATTATGAT
 AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGTTTGAA
 CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
 AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTTCCATA CGAACGGTGA ATTTTATAT
 CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
 GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
 ACGGAAAATG GCTTTATAAA ATAA

EF014-2 (SEQ ID NO:50)

MSRKRKIS LISLVIILVF VTVGSAYFAV AGSYLKKTID KGYVPIKNDY
 NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
 NYQGMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFIKLIDAV GGIDVNVKQA
 FDGVTKDGP SIHFDAGKQH LDGKALSIA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
 SIMKIMDIID SLNGNIQTDV DSNEHLHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF014-3 (SEQ ID NO:51)

TGCT

GTAGCGGGTA GCTATTTAAA GAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
AAGACGAAGA AAATAACCTA FTTAAGTTTG CCACGGGATA GTTTTGTTCA AATTGATGCG
AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAAC
TTTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
GCGTTTGATG GTGTACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAAACAG
CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTAAA GACATAGCGA TAACGATATT
ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
CAATCAATCA TGAAAAAAT GGACATTATT GATTCGTTAA ATGGAAACAT TCAAACATGAT
GTGGATTCCA ATGAAATTGAC TCATTTAGTC AAAGAAGGTT TGACTTGGAC CAATTATGAT
AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGGTTGAA
CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTCCATA CGAACGGTGA ATTTTATAT
CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
ACGGAAAAATG GCTTTATAAA A

EF014-4 (SEQ ID NO:52)

AV AGSYLKKTID KGYVPIKNDY

NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
NYQGMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFYKLIDAV GGIDVNVKQA
FDGVTKDGP SIHFDACKQH LDGKALSIA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
SIMKIMDIID SLNGNIQTDV DSNEHLHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL
YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF015-1 (SEQ ID NO:53)

TAATTAAAAA TGTGTAAAAA GGGTCTGATG AAAAAAGGAG ACATAATAGT TATTATCTTT
TTAATAGCTA TCTCTTTTTC TCCATATTTT ATTTTTTTTC ACAATAATCC ATTTAACTCC
AAAAGTTTTC ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTGAGCGT
ATAAATTTAG ATGATTCAAA AGAATTATC AAAACATATT ATCCATCAAA AGGGCAATAT
AATACTATAG AAGTTAAAAA TGGGCACGTT CGTGTAAGAA AAGATAATAG TCCAGATCAA
ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCCTCAC
AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA CTAA

EF015-2 (SEQ ID NO:54)

MK KGDIIIVIFL IAISFSPYFI FFHNNPFNSK SFDDTKYAVV KIDGKEIERI
NLDDSKFIK TTYPSKGQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
FILEIVQQYS KDYYIY

EF015-3 (SEQ ID NO:55)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAATAATCC ATTTAACTCC
 AAAAGTTTTS ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTBAGCST
 ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGJAATAT
 AATACTATAG AAGTTAAAAA TGGGCACGTT CSTGTAAAAA AAGATAATAG TCCAGATCAA
 ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNA A CTAGTATCTG TATTCTCTAC
 AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA C

EF015-4 (SEQ ID NO:56)

NNPFNSK SFDDTKYAVV KIDGKEIERI
 NLDDSKFEIK TYPSKQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
 FILEIVQQYS KDYYIY

EF016-1 (SEQ ID NO:57)

TGACGGTTGC CCCCSTCCAA TAGAAAGGAG TTTATGATGA AAAAGAAATA TTCTTTAGCC
 TTGCTGGTTA TGTGTGTAG TTTACTCCTA TTTGCAGGTT GTGGTAAAAG AAAAGCAAC
 GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCC TGGGTTTTCA AGATAAATCA GGCAAAATTG TCGGCTTTGA TGTGACTTA
 GCCAAAGCGG TTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTTGTTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT
 TCCCACGAAG ATAATTTAAA AAATATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTTCTC AAAAAATGTT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AACTAA

EF016-2 (SEQ ID NO:58)

MMKKYSLAL LVICCSLLLF AGCGKRKSNE DQWTRINEEK RIIIGLDDSF
 VPMGFQDKSG KIVGFDVLA KAVFKLYGIS VDFQPIDWSM KETELQNQTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYLS HEDNLKNYTI SHVGYDNEDF
 AVGVKSDNQ LVQKINTAFE TLRKDGTLSK ISQKWFGEVD TNNTKIN

EF016-3 (SEQ ID NO:59)

AAGCAAC
 GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCC TGGGTTTTCA AGATAAATCA GGCAAAATTG TCGGCTTTGA TGTGACTTA
 GCCAAAGCGG TTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTTGTTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCCACGAAG ATAATTTAAA AAACATATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTCTC AAAAAATGGT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AAC

EF016-4 (SEQ ID NO:60)

SNE DQWTRINEEK RIIIGLDDSF

VPMGFQDKSG KIVGFDVDLA KAVFKLYGIS VDFQPIDWSM KETELQNTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYLS HEDNLKNYTI SHVGYDNEDF
 AVGVKSDNQ LVQKINTAFE TLRKDGTLK ISQKWFGEDEV TNNTKIN

EF017-1 (SEQ ID NO:61)

TGAGGTGTTT TTATGAAAAG GGCAACAAAG CAAAGGCTGT CTTTGGCAGC AATCATGGTT
 CTACTTCTCT CGGGCTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCTGTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCTTTGA CGAAAAAGGA
 GAAGCGAAAC CAGCATGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTAAAGCTAT
 ACTTTTACGA TTGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAATGAT
 TTTGAATACT CTTGGAAGCG CACAGTGGAC CAAAAACAG CTTCCCCGCA AGCGTATTAC
 TTTGAAGGGT TAAAAAATTA TCGTGCTATT GTTGACGTA GCAATCTAA AGAAGAGTTA
 GGGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTAA ATGAAGCATT TGTGAAAAA
 ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGGTTGGG ATGGCAGCAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAAG CAATACTGGG
 AAAAACTTT TCGAAGGGAA AGAATTAGAT GTTGTAAGAA TTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAAATACGC AAAAAGATCT TTTGGCAAAT AAGAATGCAC GTCGAGCAAT AGCATATCA
 TTGAATTCTG AGCGTTTAGC TAAAAATGTT TTAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTCGAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT GGCAACGGC TAAAAAGAA
 TTAGGAATTG AAAAAAGCGA GCTAACGATT TTAAGTTCCG ATACAGAAAA TGCTAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTAG AAAAAATTAAC AGTCAATGTT
 TCACCAGTTC CTTTAAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG
 GTTGGTGGCT GGACGCCAGT ATATGCTGAT CCAATCGATT TCTTAACTT ACTGCAATCA
 AAAAAATCCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCCTAGTT CCTCTTTATC AATTAACAGA AGCAGCCTTA
 GTGGCCGATT CTGTCCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAGTA A

EF017-2 (SEQ ID NO:62)

MKRATKQ RLSLAAIMVL LLSGCGSVGK ETKKQEQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTE VELSYPMYSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGNTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD

TABLE 1 Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQGALAD NLENLTVNVS
 PVPFNNRLEK SRSGDFDITV GGWTPVYADP IDFLNLLQSK NSNNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF017-3 (SEQ ID NO:63)

CTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTGCG GGATTGATTG GGAATTATCA ACGGCAGACG TGTCGTTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCCTTTGA CAAAAAGGA
 GAAGCGAAAC CAGCATTGCT AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT
 ACTTTTACGA TTGAAAAA BA TGCAAAATGG AGTAACGGCG AGCCAATCAC A3CAAAATGAT
 TTTAATACT CTTGGAAGCG CACAGTGGAC CCAAAAACAG CTTCCCGCA A3CGTATTAC
 TTTAAGGGT TAAAAAATTA TCGTGTCTATT GTTGACGGTA GCAATCTAA A3AAGAGTTA
 GGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGST ACCAGCTTTT TATCCTTTAA ATGAAGCATT T3TCGAAAAA
 ACGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGTTGGG ATGGCAGCAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTGCTAGA TAAGGTGAT GTCCAAGTAG TTAAGAAGT CAATACTGGG
 AAAAACTTT TCGAAGGGAA AGAATTAGAT GTTGTA AAAA TTTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAATACGC AAAAAATCT TTTGGCAAAT AAGAATGCAC GTCGAGCAAT AGCATTATCA
 TTGAATCTG AGCGTTTAGC TAAAAATGTT TTAATGATG GCTCAAAAA AGCACTTGGC
 TTCGTGCAA CAGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTGCAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT G3CAAAACGCG TAAAAAGAA
 TTAGGAATTG AAAAAAGCGA GCTAACGATT TTAAGTTCCG ATACAGAAAA TGCTAAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT
 TCACAGTTC CTTTTAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATT C3ACATTGTG
 GTTGTGGCT GGACGCCAGT ATATGCTGAT CCAATCGATT TCTTAACTT ACTGCAATCA
 AAAAAATCCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCTAGTT CCTCTTTATC AATTAACAGA AGCAGCCTTA
 GTGGCCGATT CTGTCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAG

EF017-4 (SEQ ID NO:64)

CGSVGK ETKKQEQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTLE VELSYPMYSYF
 CQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYIIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD
 LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQGALAD NLENLTVNVS
 PVPFNNRLEK SRSGDFDITV GGWTPVYADP IDFLNLLQSK NSNNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF018-1 (SEQ ID NO:65)

TGTCATTACA ACGATACCAA TTTTAATCAT TTATCCATTA CTACAAAAAC ACTTTATCGG
 CGGTATGATG GCCGGTGCAG TAAAAGAATA AAGAAAGTAG GGAACAATAT GAAAAAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTAGGCGGTT TATTGGTGGC AACGGCGGTC GTTAGTTTAG CGGCCTGTAG CCGTGCGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACCTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGGATATTG AATTTATTTC CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAAC TGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTAAA CGATTTAGCT AAAAAATATG ACCCCTATTT AATGAAAGTT
GTTAACCAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCCAGTAAA TGATAATTTT
GTTATTTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC
ACCACAGTGG GCGATGGTGC AGGACCATT TTAGACAAAT TACAAGACTT CTTAGGTGTT
CCTTTAGAGG ATAAAAATGG TAAATACTAT GATCGAAAT TAGATAAAGA ATATTTAGAA
TGGTTAAAAA CATTTAATGA TGTTTACCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGAAAAAGTG AAACAAGGAA ATTATGCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAACCTC ACAGAATTGA TGAAAAATC TGGCACACGT
TATATAGCCA TTGATGGACC AAGTAGCACT TCTGGCCGAA AACCAACATT AAATCAAAACC
GGCATTTCAG GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GGAAAAATG ATTATTTACC AGAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCCTA
TACTTTAACA ACGACCGTGT CAATAAATA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
ATGCAAGAAT GGGGCAAAG AAAATTAGTC CCACATTTTCG TAATTGAAAA TATTAATCCA
GATGCAGGAA CGCCGGAAG TCGTGCGAAT GAAGCGATTG AAACCAAAT AAATACAACC
GTTATTTCAA TGATTCGTGC GAAAGATGAT AAAGCCTTTG ACAAATCTTT AGAAGACTAC
AAAGCATTCT TAAAAATCAA TAAATGGGAT GCAATTGAAA AAATAAAATC TGAGAAATG
GCGGAAAACA GAGACAACT TAAGTAA

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EF018-2 (SEQ ID NO:66)

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MKKV LGLLVATAV VSLAACSGGE
KKASSDVSIK DRYELDEKTP AWKLDKKKEP TKIKWYINSD WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMEISSG DMPDIVTLTE KTGQAALKAD SWAYSLNDLA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPDVSTPEN
FEKVMQIQKE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDEKEYLE
WLKTFNDVYR AGNISDDST DDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWLSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMEASLTQ
MQEWGKGKLV PHFVIENINP DAGTPEARAN EAIETKLNTT VISMIRAKDD KAFDKSLEDY
KAFLKSNKWD AIEKIKSEKM AENRDKLK

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EF018-3 (SEQ ID NO:67)

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CTGTAG CCGTGCGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACCTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGGATATTG AATTTATTTC CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAAC TGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTAAA CGATTTAGCT AAAAAATATG ACCCCTATTT AATGAAAGTT
GTTAACCAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCCAGTAAA TGATAATTTT
GTTATTTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ACCACAGTGG GCGATGCTGC AGGACCATTT TTAGACAAAT TACAAGACTT CTTAGGTGTT
GGTTTAGAGG ATAAAAATGG TAAATACATAT GATCGAAATT TAGATAAAGA ATATTTAGAA
TGGTTAAAAA CATTTAATGA TGTTTADCGA GCAGGCAATA TTAGTSATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGA AAAASTG AAACAAGGAA ATTATSCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAATTC ACAGAAATTTA TGA AAAAATC TGGCACACGT
TATATAGCCA TTGATGGAAC AAGTAGSACT TCTTCCCGAA AACCAACATT AAATCAAACC
GGTATTTGAG GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GSA AAAATTG ATTATTTACC ABAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCTTAC AACAAAAAAT ATGGCATTAG TCGTTTCTTA
TACTTTAACA ACGACCGTGT CAATAAAATA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
ATSCAAGAAT GGGGCAAAGG AAAATTASTC CCACATTTCC TAATTGAAAA TATTATATCCA
GATGCAGGAA CCGCGGAAGC TCGTGCGAAT GAAGCGATTG AAACCAAACCT AAATACAACC
GTTATTTCAA TGATTCTGTC GAAAGATGAT AAAGCTTTTG ACAAATCTTT ABAAGACTAC
AAAGCATTTCT TAAATCAAAA TAAATGSSAT GCAATTSAAA AAATAAAATC TBAAGAAATG
GCGGAAAACA GAGACAAACT TAAG

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EF018-4 (SEQ ID NO:68)

CSGGE

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KKASSDVSIK DRYELDEKTP AWKLDKKKEP TKIKWYINSO WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMEISSG EMPDIVTLTE KTGQAALKAD SWAYSINDLA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPVDSTPEN
PEKVMQIQIE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDEKEYLE
WLKTFNDVYR AGNISDDSFT EDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWSLSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMEALSTQ
MQEWGKGLV PHFVIENINP DAGTPEARAN EAIETKLNNT VISMIRAKDD KAFDKSLEDY
KAFLKSNKWD AIEKIKSEKM AENRDKLK

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EF019-1 (SEQ ID NO:69)

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CTTGGTTCAT TCTTACTCGC AGCTTGTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
CAATGGACAG TTGGACAAGG CAGCATTCAA GATTATTTAG CGAAAGAATT GAAAGATGTC
CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTTTGAAC TGACTTATTA
TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAATTTGCG
CCAACCTATG TAGTCAAAAA CGCGCAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
ACCAAAGGCG TCCAAGAATA TCTTGCAAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
TGGGTAAACA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AAACGCTACT
GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
CTTGTAACAA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
CCTATTGCGA ATACTCAAAT TGTGAAGAT GTAAAAAAG CGCTCTTAAA TTAA

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EF019-2 ((SEQ ID NO:70)

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MKLLKK TVLIGTTLLL GSFLAACGN TNKEANNADK THEVDTLGN KVTVPKPKR
IIASYLEDYL VALGEKPVAQ WTVGQSSIQD YLAKELKDVP TISYDLPEYA VLKFEPLDLL

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGGK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF019-3 (SEQ ID NO:71)

TTGTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
 AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
 CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
 CAATGGACAG TTGGACAAGG CAGCATTCAG GATTATTTAG CGAAAGAAAT GAAAGATGTC
 CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTGGAACC TGACTTATTA
 TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAAATGCG
 CCAACTTATG TAGTCAAAAA CGGCGAAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
 GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
 ACCAAAGGCG TCCAAGAATA TCTTGGCAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
 TGGGTAACCA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
 TATCAGGACT TAGGCCTCCA AGTTCCAAA TTAGTGGAAG AAATTTCTAA AACCGTACT
 GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
 CTTGTAAACA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
 GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
 CCTATTGCGA ATACTCAAAT TGTTGAAGAT GTAAAAAAG CGCTCTTAAA T

EF019-4 (SEQ ID NO:72)

CGN TNKEANNADK THEVTDTLGN KVTVPAPKPR
 IIASYLEDYL VALGEKPVAQ WTVGQGSIQD YLAKELKDVP TISYDLPYEA VLKFEPLDLLL
 ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGGK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF020-1 (SEQ ID NO:73)

TGAGGAGATG AGAAAATGAA AAAGGTAGTT TCAATTTTGT TGATGGTTGT TGCAGTCTTC
 ACATTAAGTG CATGTAATGG TTCTAAATTA GATAAACAG GTGAAGAATT TAAAAATTCT
 ATAATGAAAG ATTCTTCATA TGGTGATGAA TATTCAGAAG ATGGTTTATG TTTTAAATA
 TATAAAGATA AAGACACTAA TCGTTATTTG GCTGATGTTT GGGTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATGAAAGCT AGTGGAAGCT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AATAA

EF020-2 (SEQ ID NO:74)

MKKVVS ILLMVAVFT LTACNGSKLD KTGEFEKNSI MKDSSYGDEY SEDGFSFLIY
 KDKDNTNRYLA DWVVPVKDET SALEYFYFYD EDKRLDSTKS KVTFDMMKAS GNYEVVYKSG
 KFK

EF020-3 (SEQ ID NO:75)

ATGTAATGG TTCTAAATTA GATAAACAG GTGAAGAATT TAAAAATTCT

100

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATAATGAAAG ATTCTTCATA TGSTGATGAA TATTCAGAAG ATGGTTTTAG TTTTTTAATA
 TATAAAGATA AAGACACTAA TCGTTATTMG GGTGATGTTT GGGTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATCAAAAGT AGTGAAGTAT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AA

EF020-4 (SEQ ID NO:76)

CNGSKLD KTGEFKNST MKDSSYGDEY SEDGFSFLIY
 KDKDNTNRYLA DWWVPVKDET SALEFYFYIYD EDKRLDSTKS KVTFDMMKAS GNYEVVYKSG
 KFK

EF021-1 (SEQ ID NO:77)

TAGTTGTTTA AATACATTAA ACTATTTTTA GGAGGCTTTA CAGAAATGAA AAAAGCAAAA
 TTATTCGGTT TTAGTTTGAT TGCATTAGGT TTATCAGTTT CACTTGCAGC ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTCA ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGTT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC
 AACACAATCT TTGGTATTGG CTACTTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
 AACCCTGATA CAAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAAA GAATGTCGTT
 TCTGCAACAT TTAGAGATAA TGAAGCAGCT TACTTAGCCG GTGTGCTGCTG TGCATAATGAA
 AAAAAACGA ACAAAGTCGG TTTTGTGGT GGTGAAGAAG GGGTCGTAAT TGACCGTTTC
 CAAGCTGGTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTAAT
 GTTGATACGA AATATGCGGC TTCATTTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
 GCAATGTACC AAAACGGCGT TGATATCATC TTCCATGCTT CTGGTGCGAC TGGACAAGGG
 GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCCTG GCGACAAAGT TTGGGTAATC
 GCGCTTGACC GCGATCAAGA TGCTGATGGC AAGTACAAAA CAAAAGACGG CAAAGAAGAC
 AACTTCACGT TAACCTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
 CGTGCGTTAG AAGACAAATT CCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
 GCGCTTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAACAGCA
 AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCCAGAAA AACCAGAATA A

EF021-2 (SEQ ID NO:78)

MKKAKL FGFSIALGL SVSLAACGGG KGKTAESGGG KGDAAHSAVI
 ITDTGGVDDK SFNQSSWEGL QAWGKEHDL ESKGYAYIQ SNDAADYTTN IDQAVSSKFN
 TIFGIGYLLK DAISSAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
 KTNKVGTVGG EGVVIDRFQ AGFEKGVADA AKELGKEITV DTKYAASFAD PAKGKALAAA
 MYQNGVDIIF HASGATGQGV FQEAKDLNES GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
 FTLTSTLKG VTAVDQDIANR ALEDKFPGE HLTVGLKDGG VDLTDGYLND KTKEAVKTAK
 DKVISGDVKV PEKPE

EF021-3 (SEQ ID NO:79)

ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTCA ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGTT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AACACAATCT TTGGTATTGG CTAATTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
AACCCTGATA CAAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAAA GAATGTCGTT
TCTGCAACAT TTAGAGATAA TGAAGCAGCT TACTTAGCCG GTGTTGCTGC TGCAAATGAA
ACAAAAACGA ACAAAGTCGG TTTTGTGGT GGTGAAGAAG GGGTCGTAAT TGACCGTTTC
CAAGCTGGTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTACT
GTTGATACGA AATATGCGGC TTCATTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
GCAATGTACC AAAACGGCGT TGATATCATC TTCCATGCTT CTGGTGCGAC TGGACAAGGG
GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCTG GCGACAAAGT TTGGGTAATC
GGCGTTGACC GCGATCAAGA TGCTGATGGC AAGTACAAAA CAAAAGACGG CAAAGAAGAC
AACTTCACGT TAACCTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
CGTGCGTTAG AAGACAAATT CCCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
GGCGTTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAAACAGCA
AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCAGAAA AACCAGAA

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EF021-4 (SEQ ID NO:80)

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CGGG KGKTAESGGG KGDAAHSAVI
ITDTGGVDDK SFNQSSWEGL QAWGKEHDLF EGSKGYAYIQ SNDAADYTTN IDQAVSSKFN
TIFGIGYLLK DAISSAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
KTNKVGFGG EGVVIDRFQ AGFEKGVADA AKELCKEITV DTKYAASFAD PAKGKALAAA
MYQNGVDIIF HASGATGQGV FQEAADLNEG GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
FTLTSTLKV GTAVQDIANR ALEDKFPGGE HLVYGLKDG GDLTDGYLND KTKAEVKTAK
DKVISGDVKV PEKPE

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EFO22-1 (SEQ ID NO:81)

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TAAGAGCATA AAAAAATGAA GAGTTATAGG AGAAAGAAGA TGAAAAAGTA TTTAAAAATC
ACAATGGTTT GTATTTTATT GGTAGGATTT TTAGCTGGGT GTACCAATAA AAATGAAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTTT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTAGA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCATTG
CCGATGATTT CAGAAGATGG AAAAACCTAC ACGATTCTCT TGAGAAAAAG AGCGGTTTGG
AGTAACGATG ATCCTGTAC AGCACATGAT TTTGAATATG CTTGCAAAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATTCAAAA TGGTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTTGTTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAG AGTAGTCGAA CAATTGGGTG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGG TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCGCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAACGGCG CAACAGAATA AAAATAATAC GTTGTATCAT
TCGTATCCAA CAGCGACAAT GAATATTG CGCTTAAATC AAAACCGNA AGGGCAAGCN
ACGCCGCTTG CAAACGAAAA CCTGCGTAAA GCATTGGCTT TAGGAATAGA TAAAGAAAAAT
CTAGTCAATA ATATTATTGC AGATGGTTCT AAAGCGCTAC ATGGTGGGAT TACGGAAGGC
TTTGTGGCGA ATCCACAAC GGGTCTCGAT TTTCTGCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAGCAC AAGCAGAATT AGGAGAAAAG
GTTAAGCTTG AATTGATGGT AACAGATGAT GGTCTTACA AAAAAATTGG TGAAGTTTG
CAAGGCTCGC TACAAGAATT GTTTCCTGGT TTGACAATAG AGCTAACCGC ATTGCCGACT
GAAGCTGCAT TGAACCTTGG GCGAGAAAGT GACTATGATT TATCTTAAT TTACTGGACA
CCAGACTATC AAGACCCTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAAC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCTGTC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTTG CGCTCCATTA ACSTTAAAAA ATGTTTATAA GGAAAAATAA

EF022-2 (SEQ ID NO:82)

KKKYLKIT MVCILLVGF AGCTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL
KVTLKEPKPY FTSLLAPPTF FPQXKXVVEQ FGADYGTASL KVVYNGPFV KDWQQTKMDW
QLAKNNRYWD HQNVRSDIIN YTVIKETSTA LNLFDGQLE VATLSGELAQ QNKNNTLYHS
YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGAITEGF
VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELEGKV NVELMVTDDG SYKKIGESLQ
GSLQELFPGI TIELTALPTE AALNFGRESL YDLFLIYWTF DYQDPISLTM TLYKGNDRNY
QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
NFHTFGAPLT LKNVYKEK

EF022-3 (SEQ ID NO:83)

GT GTACCAATAA AAATGAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTTT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTAGA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCATTG
CCGATGATTT CAGAAGATGG AAAACCTAC ACGATTTCCT TGAGAAAAGA AGCGGTTTGG
AGTAACGATG ATCCTGTCTAC AGCACATGAT TTTGAATATG CTTGGAAAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATCAAAA TGCTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTGTGTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAA AGTAGTCGAA CAATTGGGTG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGC TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAAGTGGC CAACAGAATA AAAATAATAC GTTGATCAT
TCGTATCCAA CAGCGACAAT GAATATTG CGCTTAAATC AAAACGGNA AGGCAAGCN
ACGCGCTTG CAAACGAAAA CCTGCGTAAA GCATTGGCTT TAGGAATAGA TAAAGAAAAT
CTAGTCAATA ATATTATTGC AGATGGTTCT AAAGCGCTAC ATGGTGCGAT TACGGAAGGC
TTTGTGGCGA ATCCCACAAC GGGTCTCGAT TTTCGTCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAAGCAC AAGCAGAATT AGGAGAAAAG
GTTAACGTTG AATTGATGGT AACAGATGAT GGTTCTTACA AAAAAATTGG TGAAAGTTTG
CAAGGCTCGC TACAAGAATT GTTTCCTGGT TTGACAATAG AGCTAACCGC ATTGCCGACT
GAAGCTGCAT TGAACCTTGG GCGAGAAAGT GACTATGATT TATTCTTAAT TTACTGGACA
CCAGACTATC AAGACCCTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAACC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT
GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCTGTC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTTG CGCTCCATTA ACGTTAAAAA ATGTTTATAA GGAAAA

EF022-4 (SEQ ID NO:84)

CTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KVTLKEPKFY FTSLLAFPTF FPQNXKVVEQ FGADYGTASD KVVYNGPFV V KDWQQTKMDW
 QLAKNRYWD HQNVRSIIN YTVIKETSTA LNLFDGQLD VATLSGELA QNKNNNTLYHS
 YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGATEGF
 VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELGEKV NVELMVTDDG SYKKIGESLQ
 GSLQELFPGL TIELTALPTE AALNFGRES D YDLFLIYWTP DYQDPISTLM TLYKCNDRNY
 QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
 NFHTFGAPLT LKNVYKEK

EF023-1 (SEQ ID NO:85)

TAAATGGAG GGATCGGTAT GAAGAAATTA AAAATGTTAG GATGCGTCGG GTTGCTTTTA
 GCTTTAACGG CTTGTCAGGC GGGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
 CAAAAAATG CAATTAGTTC TGAAGCGGCT ATTTGACAA TGGAACCACA CACAGCGGGG
 GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTA
 GAAGATGAAT TAGAGTTGGG GGTCGCTGCC GAAGAACCAG CGATTCTGA AGATGAAACC
 GTTTATACAT TTAAGATTAG AGAAGATGCC AAATGGTCGA ATGATGATCC AGTAACAGCA
 AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCTA AATCAGGATC GATTTCATCA
 GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATG CTTTAGAAGG CGCAGATGTG
 AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
 ACCCTTATTT TGAAATCATT ACTTTCGTTT CCTGTTTGT TTCCACAAAA TGAATAATAT
 ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGCAGAAC ATTTGATTTA TAATGGTCCT
 TTTAAATGTA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
 ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
 CCAACGACAG CCGTGAATTT GTTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
 GGTGAATTTA TTCCTGGTTA TGTTGATAAT CCAGCCTTTC TTTCAATTCC TCAATTCGTC
 ACATACTTTT TAAAAATGAA CAGCGTTCGT GATGAAAAAG AAAATCCGGC TTTAGCGAAC
 AACAATATTC GTAAAGCGTT GGCACAAGCT TTTGATAAAG AAAGTTTGT AAAAGAAGTC
 TTGCAAGATC AATCAACGGC TACAGATCAA GTAATCCGC CGGGACAAAC GATTGCGCCA
 GATGGAACAG ATTTACACAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
 GCGAAAGCAA AAGAATTCG GGAAGGAGG AAAAAAGAAA TTGGGCTGGA TAAATCAAA
 TTAGAATTTT TAACAGATGA TACAGACAGC GCCAAAAAG CTGCTGAGTT TTTCCAATTT
 CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
 CGTGTTGATC GTGATCAAAC GAGAGACTAT GATTTAGAAT TATCTGGTTG GGGAACCGAT
 TATCGTGATC CATTACAGT TATGCGCATC TTTACTTCGG ATAGTACCTT GGGCGGCGTA
 ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
 GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
 ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
 GATCTGTATT GGCATTTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTAACTAA

EF023-2 (SEQ ID NO:86)

MKKLK MLGCVGLLLA LTACQAGTGN SADSNAKEQ KIAISSEAAI STMEPHTAGD
 TTSTLVMNQV YEGLYVLGKE DELELGVAAE EPAISEDTV YTFKIREDAK WSNDPVTAN
 DFVYAWQOVA SPKSGSIHQ LFFDVIKNAK EIALEGADVN TLGVKALDDK TLEITLERPT
 PYLKSLLSFP VLFPPQNEKYI KEQGDYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNDT
 YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVNVKLSG EFIPGYVDNP AFLSIPQFVT
 YFLKMNSVRD GKENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
 GTDFTKLAAG KNNYLTIDTA KAKEFWKGG KEIGLDKIKL EFLTDDTDSA KKAEEFFQFQ
 LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
 FKSDTYDQLI QETRTTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
 LYWHSFGPTY SLKWAYVN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF023-3 (SEQ ID NO:87)

GGGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
CAAAAAATTG CAATTAGTTG TGAAGCGGCT ATTCGACAA TGGAAACCACA CACAGCGGGG
GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
GAAGATGAAT TAGAGTTGGG GGTGCTGTCG GAAGAACCAG CGATTTCTGA AGATGAAACC
GTTTATACAT TTAAGATTAG AGAAGATGCG AAATGGTCGA ATGATGATCC AGTAACAGCA
AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCTTA AATCAGGATC GATTCATCAA
GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATTG CTTTAGAAGG CGCAGATGTG
AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
ACCCCTTATT TGAAATCATT ACTTTCGTTT CTTGTTTTGT TTCCACAAAA TGAAAAATAT
ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGAGAAC ATTTGATTTA TAATGGTCCT
TTTAAATTGA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
CCAACGACAG CGGTGAATTT GTTGACTCG AATGAATTGG ATGATGAGAA TAAGCTAAGT
GGTGAATTTA TTCCTGGTTA TGTGATAAAT CCAGCCTTTC TTTCAATTCC TCAATTCTGC
ACATACTTTT TAAAAATGAA CAGCGTTTCG GATGGAAGG AAAATCCGGC TTTAGCGAAC
AACAAATATC GTAAAGCGTT GGCACAAGCT TTGATAAAG AAAGTTTTGT AAAAGAAGTC
TTGCAAGATC AATCAACGGC TACAGATCAA GTAATTCGCG CGGGACAAAC GATTGCGCCA
GATGGAACAG ATTTACAAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
GCGAAAGCAA AAGAATTCTG GGAAAAAGG AAAAAGAAA TTGGGCTGGA TAAAAATCAA
TTAGAAATTT TAACAGATGA TACAGACAGC GCCAAAAAAG CTGCTGAGTT TTTCCAATTT
CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
CGTGTGATC GTGATCAAAC GAGAGACTAT GATTAGAAT TATCTGGTTG GGAACCGAT
TATCGTGATC CATTAAACAGT TATGCGCATC TTTACTTCGG ATAGTACCTT GGGCGGCGTA
ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
GATCTGTATT GGCATTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTTAAC

EF023-4 (SEQ ID NO:88)

GTGN SADSNAAEQ KIAISSEAAI STMEPHTAGD
TTSTLVMNQV YEGLYVLGKE DELELGVAEE EPAISEDETV YTFKIREDAK WSNDPVTAN
DFVYAWQQVA SPKSGSIHQ A LFFDVIKNAK EIALEGADVN TLGVKALDDK TLEITLERPT
PYLKSLLSFP VLFPQNEKYI KEQGDYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNDT
YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVVKLSG EFIPGYVDNP AFLSIPQFVT
YFLKMNSVRD KENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
GTDFTKLAKE KNNYLTIDTA KAKEFWEKKG KEIGLDKIKL EFLTDDTDSA KKAAEFFQFQ
LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
FKSDTYDQLI QETRTTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
LYWHSFGPTY SLKWAYVN

EF024-1 (SEQ ID NO:89)

TAATGGCCGT TCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
AACAAAGGATC AAAAAAAGG AGAAGTGAGC ATGAAAAAG TACTACCTTT TATTGCCTTA
GTCGGCTTGT TATTGTTGTC AGGTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
GGTGGTAAAT GGAAAGTGA AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
TTTTTCAGCTA ATGACTCAGA GGATAGTGT AGTGGGACAT ACACTTATGA TGAAAAAAT
AAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTCA TTATGAAAA AGTNGANTNC
AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAA
ACAGAATAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF024-2 (SEQ ID NO:90)

M KKVLPFIALV GLLLLSGCGT DMKKILTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXXKITGEIGE KQRTLIKQKT E

EF024-3 (SEQ ID NO:91)

ATT GACTGCCGAT
 GGTGGTAAAT GGAAAGTGGA AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
 TTTTCAGCTA ATGACTCAGA GGATAGTGTT AGTGGGACAT ACACTTATGA TGAAAAAAAT
 AAAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTTCA TTATGGAAAA AGTNGANTNC
 AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
 ACAGAA

EF024-4 (SEQ ID NO:92)

LTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXXKITGEIGE KQRTLIKQKT E

EF025-1 (SEQ ID NO:93)

TGAATGAAAC ATATTAAAGG AATGTTGGTT TTTATCGGAT TATTTATTTT GGTGGTTGT
 GCGCCAGATC AAGAGCCAAC GAAACAAACA ACAAGTGGTC CGCAAGAGAC AAAGCAAGTG
 AAGCAAGTTA CCGTCACCAA TCAAACGACT TCTGCGGTGG AAAAAACAAGC GCCGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGCCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAAGGTGT ATTTACTGGC GGAAATTACG GCATTGTAGA GATTATTACG
 GAACCTGAAA CGCAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TGATCCTTAT
 TATGATACAC GCTATTCGGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTCAAGCA
 AGCAACACGC GTACAGACGA TACGTTAGTC ACCGTTGTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTTACA GGTAATTTTT ATACGGTACG CGGTTTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCCTTTA GCAGCAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGGCGCTTT TTATCGTCAA TCGAAATATT
 ATTCACCAGG ATACAATAAA CAAACCAACA ATTCTTTTAT TCATTTTGTA G

EF025-2 (SEQ ID NO:94)

MKHIKMLVF IGLFILVGCA PDQEPKQTT SGPQETKQVK QVTVTNQTTS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTTFGT TPPAKYTPPE KKKKMFWSNQ PPLGLMTGNY
 YKNEGVTGG NYGIVEIITE PETQRILNVE FTEFASDPY DTRYSGVNKR LSDYPEFQAS
 NTRTDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LLFIL

EF025-3 (SEQ ID NO:95)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAC GAAACAAAACA ACAAGTGGTC CGGAAGAGAC AAAGCAAGTC
 AAGCAAGTTA CCGTCACCAA TCAAAAGCACT TCTGCGGTGG AAAACAAGC GCGGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGGCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAACTGT ATTTACTGCG CCAAAATTACG GATTTGTAGA GATTATTACG
 GAACCTGAAA CCGAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TATCCTTAT
 TATGATACAC GCTATTCGGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTTCAAGCA
 AGCAACACCG GTACAGACGA TACGTTAGTC ACCCTTCTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTACA GSTAATTTTT ATACGGTACG CGSTTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCTTTA GACACAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGCGCCTTT TTATCGTCAA TCGAAATATT
 ATTCACCAGG ATACAATAAA CAAACCAACA ATTCTTTTAT TCATTTTG

EF025-4 (SEQ ID NO:96)

TKQTT SGPQETKQVK QVTVTNQTTS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTFGT TPPAKYTPPE KKKKMFWSNQ PPLGLMTGNY
 YKNEGVTGG NYGIVEIITE PETQRILNVE FTEFASDPY DTRYSGVNKR LSDYPEFQAS
 NTRTDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LLFIL

EF026-1 (SEQ ID NO:97)

TGAGTGTATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAAATAA
 TTTTTTGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTTGCTTAG TGCTTGTTCA TCTGATAAAA AAACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACCT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAATTAA

EF026-2 (SEQ ID NO:98)

MKMSK VLTTVLTATA ALVLLSACSS DKKTDSSSSS
 KETANSSTEVS GASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSNFNIVH GTVKGDIKVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF026-3 (SEQ ID NO:99)

AACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACCT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCAACGATG TCTATCGTAA ATTAGCACTT TATTCCCAAG ATGATAATAA AAAAGTAAC
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAAT

EF026-4 (SEQ ID NO:100)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF027-1 (SEQ ID NO:101)

TTTGGTATGA AACAGAAAAA GTGGTTAATC GGACTTGTTC CACTGGGCTT GGTTTTAGCA
 GCATGTGGAA GTGGCGGTTT GAAAACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAACCT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCGA TCCAGCATAC GGTTCAGTA GCAGTAATCA AATGGATATT
 TTTAAAAATG GCGTGCCTG GCGGGAAGGA CAAGCCACGA TGAAGAATT TGGTGTCAAA
 GCAATCGATG ACCAGACACT AGAACTAACA TTGGAAAAATC CAATTCCTTA TTTAGCCCAA
 GTCTTGGTTG GGACACCTTT TATGCCATAA AATGAAGCCT TTGCCAAAGA AAAAGGTACT
 GCCTATGGGA CTTCTGCAGA TAATTTTGTG GGCAATGGGC CGTTTGTAAAT TTCAGGTTGG
 GATGGCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
 GTAAAATTGA ATGAAATTGA TGTTCAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
 TTTGATAATG GCGACTTAGA TTACACTGTT TTAGCAGATA CTTATGCACT TCAGTATAAA
 GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCCATGGTGG GTTATTTAAG CCCCATCAT
 CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
 GAAACTTTTG CAAAAGAAAT TTTAGGAGAT GGCTCGACAG CTTTAAATGG NTTGTACCA
 GCTAATTTTG CAAAAATCCA GATACAGGTG AAGATTTCG CAAAGAAAAT GGTGATTAT
 TGCCATATAA TATTAAAGAA GCCCAAGCTA ACTGGAACAA TT

EF027-2 (SEQ ID NO:102)

MKQKKWLI GLVALGLVLA ACGSGGSKTT SNEPATQKIN VASGGELSTL DSAHYTDVYS
 SDMIGQVVEG LYRQDKNGDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPKAGDFV
 AFRNVVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFVVK AIDDQLELT LENPIPYLAQ
 VLVGTPFMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
 VKLNEIDVQV VKEIGTGANL FDNGDLDTV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
 RREITGNEHV RKAFLQAIDK ETFAKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMVIY
 CHILKKPKL TGTI

EF027-3 (SEQ ID NO:103)

AACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAACCT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCGA TCCAGCATAC GGTTCAGTA GCAGTAATCA AATGGATATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTTTAAATATG GGGGTGGGT GCGGGAAGGA CAAGCCACGA TGAAGAATT TGGTGTCAAA
GCAATCGATG ACCAGACACT AGAACTAACA TTGGAATATG CAATTCCTTA TTTAGCCCCAA
GTCTTGCTTG GACACCTTTT TATGCTTAAA AATGAAGCCT TTGCCAAAGA AAAAGGTACT
GCCTATGGGA GTTCTGAGA TAATTTTGTT GCGAATGGGG CGTTTGTAAT TTCAGGTTGG
GATGSCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
GTAAATTTGA ATGAAATTGA TGTTCAAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
TTTGATAATG GCGACTTATA TTACACTGTT TTACGAGATA CTTATGCACT TCAGTATAAA
GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCGATGCTGG GTTATTTAAG CCCCAATCAT
CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCCT TTTTACAAGC GATTGACAAA
GAAACTTTTG CAAAAGAAAT TTTAGGAGAT GCGTCGACAG CTTTAAATGG NTTTGTACCA
GCTAATTTTG CAAAATCCA GATACAGGTG AAGATTTCCG CAAAGAAAAT GGTGATTTAT
TGCCATATAA TATTAAAGAA GCCCAAGCTA A

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EF027-4 (SEQ ID NO:104)

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TT SNEPATQKIN VASGGELSTL DSAHYTDVYS
SDMIGQVVEG LYRQDNKNDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPVKAGDFV
AFRNVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFQVK AIDDQTLLELT LENPIPYLAQ
VLVGTPEMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
VKLNEIDVQV VFEIGTGANL FDNGLDYTV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
RREITGNEHV RKAFLQAIK EFAKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMIY
CHILLKKPKL

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EF028-1 (SEQ ID NO:105)

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TAACAGAAGC AATACAACAA CTTAACACTT TGTTTACTTG TTATTTATCA GAAATCAACT
AAGACTTGTT ATAGTCAATG TATGGGTAGA TATGAAGGAG GAAACAAGGA AATGAAGAAA
AGAGCTTTGC TAGGGGTAC CTTATTAACA TTCACAACAT TAGCGGGTTG TACAAATTTA
TCTGAACAGA AAAGCGGCGA AAAACAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
GAAAAAGCAT CAGTAAAAAA TGTTATTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTCC CCAAACAGCT
TTTGATACCT ATTTGGTCCG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAATGTC
ACCGATTGAG CTTCCGCAGC GACAGCGATG GCTGCCGGAG TGAAAACCTA TAATAATGCT
ATTGCACTCG ATAATGACAA GTCCAAAACA GAAACAGTGC TCGAACGTGC GAAAAAAGTG
GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
GGCGCACATA ATGTTTCACG CAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
CAAATCGACG GACAACACAA AGTCGATGTG TTACTTGGCG GCGGCTCCGA ATTATTTGCC
CGGAAAGATC GTGATTTAGT CAAAGAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGGCGGG
CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
GCTCTTCAAC GGTTAGATAA AAATGAAAAA GGTTTCTTTT TAATGGTTGA AGGTAGTCAA
ATTGATTGGG CCGGGCATAG CAATGATATT GTTGGCGCGA TGAGCGAAAT GCAAGACTTC
GAAGCGGCGT TTGAAAAGGC CATCGATTTT GCCAAAAAAG ATGGTGAACA TTGGTGGTTA
CAACTGCAGA TCATTCAACA GGGGGCTTGT CTTTAG

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EF028-2 (SEQ ID NO:106)

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MKKR ALLGVTLTLT TLAGCTNLS
EQKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
DTYLVGQQAT YPEDEEENV DSASATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
KSTGLVATSE ITHATPAAYG AHNVSRRNMA EIADDFDDQ IDGQHKVDVL LGGSELFFAR
KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
LQRLDKNEKG FFLMVEGSI DWAGHSNDIV GAMSEMDFE AAFKAIDFA KKDGEHWWLQ

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LQIIQQGACL

EF028-3 (SEQ ID NO:107)

ACAGA AAAGCGGCGA AAAACAAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
 GAAAAAGCAT CAGTAAAAAA TGTTATTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
 ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTCC CCAAACAGCT
 TTTGATACCT ATTTGGTCGG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAATGTC
 ACCGATTTCAG CTTCCGCAGC GACAGCGATG GCTGCCGGAG TGAAAACCTA TAATAATGCT
 ATTGCACTCG ATAATGACAA GTCCAAAAACA GAAACAGTGC TCGAACGTGC GAAAAAAGTG
 GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
 GGGCGACATA ATGTTTCACG CAAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
 CAAATCGACG GACAACACAA AGTCGATGTG TTAATTGGCG GCGGCTCCGA ATTATTTGCC
 CGGAAAGATC GTGATTTAGT CAAAGAATT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
 AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGGCGGG
 CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
 GCTCTTCAAC GGTTAGATAA AAATGAAAAA GGTTCCTTT TAATGGTTGA AGGTAGTCAA
 ATTGATTGGG CCGGGCATAG CAATGATATT GTTGCGCGCA TGAGCGAAAT GCAAGACTTC
 GAAGCGGCGT TTGAAAAGGC CATCGATTT GCCAAAAAG ATGGTGAACA TTGGTGGTTA
 CAACTGCAGA TCATTCAACA GGGGGCTTGT CTT

EF028-4 (SEQ ID NO:108)

QKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
 DTYLVGQQAT YPEDEEENV DSASAATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
 KSTGLVATSE ITHATPAAYG AHNVSRKNMA EIADDYFDDQ IDGQHKVDVL LGGSELFAR
 KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
 LQRLDKNEKG FFLMVEGSQI DWAGHSNDIV GAMSEMQDFE AAFEKAIDFA KKDGEHWLWQ
 LQIIQQGACL

EF029-1 (SEQ ID NO:109)

TGAAGGAGGG AGAAAATGAA AAAGTTAATC GGTAAAAAGT GGCTGCTGCT TACAGCAGTA
 GCCACTTTTT TATTATCAGG ATGCGCAAGT CTTGAACAAA AAGCACAGGA TAGTGTAATA
 GAAGTTACTG AAAATGTTAC TCAAACATATT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAAAAATTG ACGGAAAAGA ACAAAGGTT
 CGGTTTTTAT TAATTGACAC ACCCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCGTTT
 GGATTGGAAG CTAGCAAACG CACAAAAGAG CTTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGGCGATAA AACAGATCGT TACGGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGGCAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACCAGGT TATGTGACAC AACGGGGGTT TAGTAAATAA

EF029-2 (SEQ ID NO:110)

MKKLIG KKWLLTAVA TFLLSGCASL EQKAQDSVKE VTENVQTIS NDQRIPADTV
 RHVDGDTTVL KIDGKEQKVR FLLIDTPETV KPCTKVQPFQ LEASKRTKEL LSTASEITFE
 YDKGDKTDY GRALGYIFVD GTLLQKTLVS EGLARVAVVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF029-3 (SEQ ID NO:111)

AAATGTTAC TCAAACATATT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAAAAATTG ACGGAAAAGA ACAAAGGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGTTTTTAT TAATTGACAC AGGCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCCGTTC
 GGATTGGAAG CTAGDAAACG CACAAAAGAG TTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGCGGATAA AACAGATCGT TACCGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGCGAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACGAGGT TATGTGACAC AACGGGGGTT TAGTAAA

EF029-4 (SEQ ID NO:112)

NVTQTIS NDQFIPADFV
 RHVGDGDTVL KIDGKEQKVR FLLIDTPETV KPKTKVQPFQ LEASKRTKEL LSTASEITFE
 YDKGDKTDYR GRALGYIFVD GTLLQKTLVS EGLARVAYVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF030-1 (SEQ ID NO:113)

TGATTGACAC ATAGGGGAGAA TAGTATGAAA AAGTTAAAAA TGATGGGGAT TATGTTATTT
 GTTAGTACCG TCTTGGTAGG TTGTGGCACA ACAGCAGANA CAAAAATAGA CGAGAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG
 CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTGGCGTAA ATTAGCGAAT
 CCCAAAAACC AAGCCCAATTA CTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTCCAC AAAACGAAGC ATTCGTGAAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCG
 TGGGATTTTG TGCCTAATCC CTACTATTAC GATAAAGAAA AAGTAAATC AGAAACGATT
 CATTTTGAAG TTTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTTG CAAATGAGAA TGTCCGCAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTACG AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTCTGCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT GATAGTGACC GA

EF030-2 (SEQ ID NO:114)

MKK LKMMGIMLFV STVLVGCCTT AXTKIDEKAT EKTSVSKKVL NLMENSEIGS
 MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIFAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPPEL GVKALDDYTL
 EVTLEKPVYP FTSLALFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYYD KEVKVSETH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDYEA
 IERSKVYSLR LNQKRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDF RQEAGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDGD SDR

EF030-3 (SEQ ID NO:115)

GAGAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTTGGCGTAA ATTAGCGAAT
 CCCAAAAACC AAGCCAATTA CTTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTTCACAC AAAACGAAGC ATTTCGTGAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCC
 TGGGATTTTG TGCCTAATCC CTACTATTAC GATAAAGAAA AAGTAAATC AGAAACGATT
 CATTTTGAAG TTCTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTGT CAAATGAGAA TGTCCGCAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTAGC AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTCTCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT

EF030-4 (SEQ ID NO:116)

EKAT EKTSVSKKVL NLMENSEIGS

MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIPAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPEEL GVKALDDYTL
 EVTLEKVPY FTSLLAFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYD KEKVSETIH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDYEA
 IERSKVYSLR LNQKRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDE RQEGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDG

EF031-1 (SEQ ID NO:117)

TGAGAAATTA GTTATTTTAG AAAAATAAAA ACCATTTTGG AGGAAGATTT AAAAATGAAA
 AAACGCGTAA TTTTAGGGAC ATTACTCGCT GCAACGTTAT TAATGACTGC TTGTGGAAAC
 AGCGAAGCAA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCGGATTAA GTGAAGATAT TGTCAAAAAA GACATTATCG CTCCATTTGA AAAAGAGAAAT
 GAAGCGAAAG TTACCTTGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAAAAAAT
 AATCCCAATG CGGGAATTGA TGTCAATTGA TTAGCACAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAAGTAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTT TGAAAGTGGT GCTGGCGTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAAACTGGGA TGAATTATGG
 TCAGCTGATT TGAAAGGTAA AATTTCTGTT CCAGACGTTG CCACGACGGC AGGTCTTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGGT CAAGATATTA CAAAAGATAA CGGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTTAAACCA AACGTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGGTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGGC
 GTTGATATTA TTCAAGGCGC ACAGAAAACG TGA

EF031-2 (SEQ ID NO:118)

MKK RVILGTLVAA TLLMTACGNS EATTKSESKG GSNALVVSTF

GLSEDIVKDD IIAPEKENE AKVTLEVGN ADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAKEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDDLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYSSSSD
 LANMFQSGEI EAAVADFV DIIQGAQKT

EF031-3 (SEQ ID NO:119)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCCGATTAA GTGAAGATAT TGTCAAAAAA GACATTATCG CTCCATTGTA AAAAGAGAAT
 GAAGCGAAAG TTACCTTAGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAAAAAAT
 AATCCCAATG CGGGAATTGA TGTCAATTGAA TTAGCACAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAASTAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTTT TBAAGTGGT GCTGGCCTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAAACTGGGA TGACTTATGG
 TCAGCTGATT TGAAGGTAA AATTTCTGTT CCAGACCTTG CCACGACGGC AGGTCCTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGCT CAATATATTA CAAAAGATAA CCGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTAAAACCA AACCTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGCTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGGC
 GTTGATATTA TTCAAGGCGC ACAGAAAA

EF031-4 (SEQ ID NO:120)

TTKSESKG GSNALVVSTF
 GLSEDIVKDD IAPFEKENE AKVTLEVGNL ADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDLLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYSSSD
 LANMFQSGEI EAAVVADFAV DIIQGAQK

EF032-1 (SEQ ID NO:121)

TGAATAAATT ATTTAGGAGG AATTATGATG AAAAAATTAA TTAGTTTAGG ATTGGTTTGT
 GTTTGTGGTA TTCTACTACT TACTGCTTGT NCGGGAAATA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAAGA CTTTGTGGCG
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAACT
 CAACTAGATG ATAAATCGAG CATAGTTCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTTCG AAACCTGCCG CAAAGATTTT GTTGTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAGTAG TAGCCAAGAT AATAACAAT CTGATGTATC TGAAAAAATA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GGTA

EF032-2 (SEQ ID NO:122)

MK KLISLGLVCV CGISLLTACX GNNDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKDID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDITL
 TFETADKDFV VRFLNEKDFQ EYMKNPVSST ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTLPSEDKN TNDITKLADE PTLEQQTVLD TLAKHQFNDM YPYKSGKMH
 IIGVIPTMDA KRW

EF032-3 (SEQ ID NO:123)

TA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAAGA CTTTGTGGCG
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAACT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAACTAGATG ATAAATCGAG CATAGTTCCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTCG AAACCTGCCGA CAAAGATTTT GTTGTTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAAAGTAG TAGCCAAGAT AATAACAAT CTGATGTATC TGAAAAAAA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GG

EF032-4 (SEQ ID NO:124)

NDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDITL
 TTFETADKDFV VRFLNEKDFQ EYMKNPVSSST ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTLPSEDKN TNDITKLADE PTLEQQTVLD TLAKHQFNDM YPYKSGSKMHS
 IIGVIPTMDA KRW

EF033-1 (SEQ ID NO:125)

TGACTGCTTT TTTTCTATTG GAGAAAAAAG TGGTTTTTTT GTATTGTTTT GACGTTGAGA
 CAAAGGAGGT TCATTTCAGA AAATTTTCCC CAAAATAAAA TAGACGAATG CGAGGATGAA
 AAAATGAAAA AATTTACTTT AACAAATGATG ACTTTAGGTT TAGTAGCAAC ACTTGGCTTA
 GCAGGATGTG GTAAACAGGA AAAGAAAGCA ACTACCTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAGTG ATTGAAGACT TAGGTAAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTCGATGC CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTTTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAGT GTTTGGAAGC AAGTGGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

EF033-2 (SEQ ID NO:126)

MKKFTLTMMT LGLVATLGLA
 GCGKQEKAT TSSEKTEVTL PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDAAEKLI ALKPQIVYVN DINLASSESV WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADSLSEHEKG QKLIKTMDE IDE

EF033-3 (SEQ ID NO:127)

CTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAGTG ATTGAAGACT TAGGTAAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTCGATGC CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTTTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAGT GTTTGGAAGC AAGTGGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF033-4 (SEQ ID NO:128)

SSEKTEVTL PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTTM TDLKKLPQMD MMAVDAEKLI ALKPQIVVYN DINLASSESV WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADLSEHEKG QKLIKTMQGE IDF

EF034-1 (SEQ ID NO:129)

TAGGAGGGAG TAATCATGAA AAAAATCGGG TATTTTAGTT GTATTATTTT TTTCATGTTT
 TTGSTAGGTT GTAGTAATAA CAAAAAAGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGACAAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-2 (SEQ ID NO:130)

MKKIGY FSCIIFMFL VGCSNNKKN GNLLNASSFP LILTTIEKE EDLTGSIFF
 NKDKTMTLEK EYLVNPNED TKKTSRTEKK VYKNIQEN KESYEIIGQL DKKTCKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF034-3 (SEQ ID NO:131)

AGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGACAAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-4 (SEQ ID NO:132)

KEN GNLLNASSFP LILTTIEKE EDLTGSIFF
 NKDKTMTLEK EYLVNPNED TKKTSRTEKK VYKNIQEN KESYEIIGQL DKKTCKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF035-1 (SEQ ID NO:133)

TAAACGAGAG GTGAGTTTAT GAAAACAAAA ATCGGAAAAA CAGTTATCTT GTCAGCATTT
 TTATTCACAA GTTTCCTTTT ACTGAGTGGT TGTACCTCGG CTGGCGAAGA GATGGAAAAA
 ACAATTGATC GACAGAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTAATGAGTA A

EF035-2 (SEQ ID NO:134)

MKTKI GKTVILSAFL FTSFLLLSGC TSAGEEMEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRS LDSQEDK IDTTE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF035-3 (SEQ ID NO:135)

GATGGAAAAA

ACAATTGATC GACAGAAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTACTGAG

EF035-4 (SEQ ID NO:136)

MEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRLDSQEDK IDTTE

EF036-1 (SEQ ID NO:137)

TAATTTTCAA GTCCTACATA TAATGGTAAA ATAGAATGGA TTGAAATTAA TTGGAGGAAT
 AATGAATCGA TGAAAAAAG ATTGCTATTA TTTATTGGTT TGGCAAGTAT ACTTACTTTG
 ACAGGATGTG CAAAATGGAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTTGTAG GTGAAGTAAC AAAGTGGAAA
 GAAGTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCGG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAAACAG CCATTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC
 GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTGTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA ATAA

EF-36-2 (SEQ ID NO:138)

MKKRLLLF IGLASILTTLT GCAKWIDRGE SITAVGSSAL
 QPLVETASEE YQSQNPRFI NVQGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVNKNVGK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAQEQD SSGMVRISVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNNKWI WSYEYMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF036-3 (SEQ ID NO:139)

GAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTTGTAG GTGAAGTAAC AAAGTGGAAA
 GAAGTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCGG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAAACAG CCATTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC



TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCCA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA A

EF036-4 (SEQ ID NO:140)

IDRGE SITAVGSSAL

QPLVETASEE YQSQNPGRFI NVQGGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVNKNVGK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAEQD SSGMVRISVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNKNWII WSYEHMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF037-1 (SEQ ID NO:141)

TGAGTGATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAATAAA
 TTTTGTGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTGCTTAG TGCTTGTTCA TCTGATAAAA AAACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAA

EF037-2 (SEQ ID NO:142)

MKMSK VLTTVLTATA ALVLLSACSS DKKTDSSSSS
 KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF037-3 (SEQ ID NO:143)

AACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA A

EF037-4 (SEQ ID NO:144)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSENFNIVH GTVKGDIEVK ANGFTLNGTK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF038-1 (SEQ ID NO:145)

TAATGGCCAT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAAATGGCG TTGGCAATGG
 AACAAGSATC AAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
 GTCGGCTTGT TATTGTGTC AGGTTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAATAAT GGAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGTCTTTG A

EF038-2 (SEQ ID NO:146)

M KLLKWRWQWN KDHKEGEVSM KKVLPFIALV GLLLLSGCGT DMKKILTADG
 GKWELENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKX NKRCL

EF038-3 (SEQ ID NO:147)

TTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAATAAT GGAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGTCTTTG A

EF038-4 (SEQ ID NO:148)

CGT DMKKILTADG
 GKWELENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKX NKRCL

EF039-1 (SEQ ID NO:149)

TAAATATATC AAAAAGAAAA AAGGGGATTA CCAACCATGA AAAAGAAAAA AGTTTTTAGT
 GCGCTTACCT TATTAACCTT TAGTACGTTG TTGATTGCAG GCTGTGCTGG CGGAGCCAAC
 TCTGCAACAG ATAAATCAAG TGCAGCTAGC TCAAGCACTG CAGTCTCTAG TTCAGCAGAA
 GCAGCTAAAG AGCAATCAAA AGGACAAGAA TTAACAGAAA TTTTATCCAG TACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAAATNAT AATAATTTAA CAGCAGAAAA TGCTAATTTT
 ATTGGTTTTAG CAAAATATGA TGGTGAAACA GGTTTTTATG AATTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTCCG ATACACAAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTTAGAA
 ACAGAACTG CCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGGAATGGCA CGAAAGTTT AGATGAAGAC GGTAACGATG TTACTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAAA ACAAGTAAAT ATGAATTCCT TGATTTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATAA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAT
 GATAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAAGTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-2 (SEQ ID NO:150)

MKKKKVFSALTLTTFSTLLIAGCAGGANSATDKSSAASSSTAVSSSAEA
 AKEQSKGQELTEILSSTDWQGTKVYDKNXNLTAEANANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFFVTDDGEKRILISDTQNYQAVVDLTEVTKDKFTYKRMGKDKDGKDVEVFVE
 HIPYSDEKLTFTNGRKDLETETGKIVTNPEGDDILGATLWNGTKVLDEGNDVTEANKMF
 ISLAKFDNKT SKYEFFDLETGKTRGDFGYFQVIDNNKIRAHVSIGDNKYGAALELTELND
 KRFTYTRMGKDNNGKEIKVFVEHEPYEGDFTPDFTF

EF039-3 (SEQ ID NO:151)

TGCAACAGATAAATCAAGTGCAGCTAGCTCAAGCACTGCAGTCTCTAGTTCAGCAGAA
 GCAGCTAAAGAGCAATCAAAAGGACAAGAA TTAACAGAAA TTTTATCCAGTACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAATNAT AATAATTTAA CAGCAGAAA TGCTAATTTT
 ATTGGTTTAG CAAAATATGA TGGTGAACA GGTTTTATG AATTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTTCGG ATACACAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTAGAA
 ACAGAACTG GCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGAATGGCA CGAAAGTTT AGATGAAGAC GGTAAACGATG TTAGTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAA ACAAGTAAAT ATGAATCTT TGATTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAT
 GATAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAAGTC
 TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-4 (SEQ ID NO:152)

ATDKSSAASSSTAVSSSAEA
 AKEQSKGQELTEILSSTDWQGTKVYDKNXNLTAEANANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFFVTDDGEKRILISDTQNYQAVVDLTEVTKDKFTYKRMGKDKDGKDVEVFVE
 HIPYSDEKLTFTNGRKDLETETGKIVTNPEGDDILGATLWNGTKVLDEGNDVTEANKMF
 ISLAKFDNKT SKYEFFDLETGKTRGDFGYFQVIDNNKIRAHVSIGDNKYGAALELTELND
 KRFTYTRMGKDNNGKEIKVFVEHEPYEGDFTPDFTF

EF040-1 (SEQ ID NO:153)

TAGATTAGAA CCACTGGAGA AAAATCTCAT ATTTCTCTCG AGGAAAGGAA GTTGAGCACA
 ATGAACAAAA AATTTTAAAT GGGGCTATTA AGTGTCGTGA CCATTCCATT ACTTGCTGCG
 TGTCAAGGAG GAGAAACACC TTCCGCAGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AACTGAAAG CACCAAGTACA ACCCGTTCCG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAAGTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAATT TTACAAGATA CTACTTATCA AGTGGATGAA
 GTCGACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTC ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCTATCTTT ATCGGGGAGC GCAAGGACGT ACGGAGATT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAAATG ACTTTGGCTA TACAGCATTG ATTGAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACTTTACC AAGATATTGT AAAATTGTTA ATGGAAAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTTTAG TACAGTACAA CTAA

EF040-2 (SEQ ID NO:154)

M NKKILMGLLS VVTIPLAAC QGGETPSAAS KNSQTVTTQS
 SAKTESTSTT RSVAQTSKE EVKEPMKTYE VGALLEAANQ RDTKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRRT EILAYMLKHA
 TPELNKHNRY GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF040-3 (SEQ ID NO:155)

AGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AAACGTAAAG CACCAGTACA ACCCGTTCCG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAASTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAAT TACAAAGATA CTACTTATCA AGTGGATGAA
 GTCSACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTC ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCTATCTTT ATGCGGGAGC GCAAGGACGT ACGGAGATT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAAATG ACTTTGGCTA TACAGCATTG ATTGAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACTTTACC AAGATATTGT AAAATTGTTA ATGGAAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT
 AAAATTTTAG CACAGTACAA C

EF040-4 (SEQ ID NO:156)

AS KNSQTVTTQS
 SAKTESTSTT RSVAQTSKE EVKEPMKTYE VGALLEAANQ RETKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRRT EILAYMLKHA
 TPELNKHNRY GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF041-1 (SEQ ID NO:157)

TAATTATTAA NTTCTGATTT TTCAGAAAAT ACAGATTGCA TTATTTTAGG AGGCAACACT
 ATGAAATTGA AAAAGTCATT AACATTCGGT GTGATTACAT TATTTAGCGT AACAACTTTA
 GCGGCTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
 AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
 CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
 TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
 GATGGACTAA CATAAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CGGTAAACCA
 GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
 GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
 GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
 AAAGCAACAC CATACTTTGA TTAATTATTA GCTTTCCCAT CATTCTTCCC GCAACGTCAA
 GACATTGTGG AAAAATATGG TAAAAATTAT GCATCAACA GCGAAAGTGC TGTCTACAAT
 GGTCCATTG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
 AAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
 GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
 CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTGTAGT TCAAAAAGAA
 GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACTTACGTA AAGCAATTTC TTACTCAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-2 (SEQ ID NO:158)

M KLKKSITFGV ITLFSVTTLA ACGGGGTSDDS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGYRL DKDNKVQPAG AAKEAEVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESA VYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTDVVVL
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF041-3 (SEQ ID NO:159)

TTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
GATGGACTAA CATACAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CGGTAAACCA
GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
AAAGCAACAC CATACTTTGA TTACTTATTA GCTTTCCCAT CATCTTCCC GCAACGTCAA
GACATTGTGG AAAAATATGG TAAAAATTAT GCATCAAACA GCGAAAGTGC TGTCTACAAT
GGTCCATTCG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
AAAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTGTGTAG TCAAAAAGAA
GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCG
AACTTACGTA AAGCAATTTC TTACTCAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-4 (SEQ ID NO:160)

CGGGGTSDDS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGYRL DKDNKVQPAG AAKEAEVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESA VYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTDVVVL
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF044-1 (SEQ ID NO:161)

TAAGATAAAA TTAGTTATAG CGTCTATAGG AGGAATAGTA TGAAAAAATT AGTTTGTGTT
ATTTTAGTTA TTTTTTTAAAC AGGTGTAGT TCTCAAAAAG CGAATGAACC TAAAAACAA
GAAAATTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATTA CAGTTCTAGC
ATAGAAACAA GCTCTAATAA TAAACTAAAA GAAACTTCAG AAAGTGCCAG CACCCTCAA
ACTTCGTCAG AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
GCAACACCTT ATGCTGTCGA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
GGAATGAATG TGCCAACCTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
TTCCGAACCTA AATTGTTTGG GGCTGAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC G3CCGATAAC
 AGTATTCGCA CCGTTAAAST AAATACAGAA TTAATTTTAG GAACTAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGB CACTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAAT AA

EF044-2 (SEQ ID NO:162)

MKKLVCVI LVIFLTGSS QKANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITLE NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTL ILGTNISSND EQNRSGTLYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF044-3 (SEQ ID NO:163)

TTGTAGT TCTCAAAAAG CGAATGAACC TAAAAAACAA
 GAAAATTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATT AAGTTCTAGC
 ATAGAAACAA GCTCTAATAA TAACTAAAA GAACTTCAG AAAGTGCCAG CACCACTCAA
 ACTTCGTCAA AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
 GCAACACCTT ATGCTGTCCA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
 GGAATGAATG TGCCAACTTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
 TTCCGAACTA AATTGTTTGG GGCTGAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT
 GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC GGCCGATAAC
 AGTATTCGCA CCGTTAAAGT AAATACAGAA TTAATTTTAG GAACTAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAA

EF044-4 (SEQ ID NO:164)

CSS QKANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITLE NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTL ILGTNISSND EQNRSGTLYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF045-1 (SEQ ID NO:165)

TAGCCAAAAA ATGAGGGAGG AAAAGAGATG AACAAGAAAC GGATTTTAGG TGCAATCACG
 TTAGCTTCTG TGTTAGTATT CGGGTTAGCT GCATGTGGTG GCGGCAATAA AGGCGGGGGC
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TGCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAATTTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAATT AGATAAATTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGTTCAAAT CTGTTCCCTTC TGCGAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCAATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA
 GACGTAGACG GCGATGGCAT TCGCGAAGAC AAAGAAGGCA AACCCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCACTTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTG GCTTAAACGT AACGTATACA ACAGGACGCT TAATTGATTT CCAAGCATT
 TATGATAAAT TGAAAAATGA TGACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTTCAGATC CTTCACCAAC CGGCTTATAT GGTCCAAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAAATC TAAATTACTT GATGCGATTG ATTCAAAAGC ATCATTTGAT
 GAAGAAAAAC GTAAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAATAA

EF045-2 (SEQ ID NO:166)

MN KKRILGAIL ASVLVFLAA CGGNGKGGN KATETEDISK MPIAVKNDKK
 AIDGGTLDVA VVMDTQFQGL FQQEFYQDNY DAQYMLPTVQ PLFNNDAFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GKDVTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPTISGI EKVDNKEVKI TYKEVHPGMQ QLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHYG GGKPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYP TYKDTEGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLIPPV FKSLHDSEAK GYTLDLKAK KLLDDAGYKD
 VGDGIREDK EGPKEIKFA SMSGGETAQP LADYYVQWK EIGLNVYTT GRLIDFQAFY
 DKLNDDPEV DLYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSASFDE
 EKRRKAFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF045-3 (SEQ ID NO:167)

ATGTGGTG GCGGCAATAA AGCGGGGGG
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCAACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TGCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAAT AGATAAATTA
 GTGTTCAAAT CTGTTCCCTC TGCGAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCAATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA

TABLE 1 Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACGTAGACG GCGATGSCAT TCGCGAAGAC AAAGAAGSCA AACCACCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGSCGA AACTGCACAA CCACCTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTS GCTTAAAGCT AACGTATACA ACAGGAGGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA T3ACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTCAGATC CTTCACCAAC CGGCTTATAT GGTTCAAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAATAC TAAATTACTT GATGCGATTG ATTCAAAAGC ATCATTTGAT
 GAAGAAAAAC GTAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAA

EF045-4 (SEQ ID NO:168)

CGGGNKGGG: KATETEDISK MPIAVKNDKK
 AIDGGTLDVA VVMDTQFQGL FQGEFYQDNY LAQYMLPTVQ PLFNNDADFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GHDVTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPTISGI EKVNDKEVKI TYKEVHPGMQ QLGCGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHY GSKPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDITY TYKDTEGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLLIPPV FKSLHDSEAK GYTLDLKAK KLLDDAGYKD
 VDGDCIREDK EGKPLEIKFA SMSGGETAQP LADYYVQQWK EIGLNVYTT GRLIDFQAFY
 DKLNDDPEV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSASFDE
 EKRKKAIFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF046-1 (SEQ ID NO:169)

TAGGAGGATA TAATGAAAAA AAAACTTATT CTACTATTGT TAGCCTTATT TTAAACGGCA
 TGTAAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAATA CCCAGTCTTC TAAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

EF046-2 (SEQ ID NO:170)

MKKKLIV LLLALFLTAC SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITIEETEN LKNRELNPTD DVSKTRRQLY EQGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF046-3 (SEQ ID NO:171)

A

TGTAAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAATA CCCAGTCTTC TAAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF046-4 (SEQ ID NO:172)

C SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITTIETTEN LKNRELNPTD DVSKTRRQLY EGGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF047-1 (SEQ ID NO:173)

TAGGGAAAAC AAGGAGGAAT TCTTATGAAA AAGATAGGGC TTATTTCTAG TGCTTTTCTT
 TTAACCCCTTG CTTTAGCAGC ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAAGTGCAG CGACAACCTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCACT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTCTTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCGAA TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-2 (SEQ ID NO:174)

MKK IGLISSAFLL TLALAACGGG KSTENTDSRS SAAESTTVES TKASATKES
 SKATTKSSDA KPSGTTTADS KATASSTKEA ANNGSAEKQS PAKNANPDDQ ANQVLNQLAN
 MFPGQGLPQA ILTSQTNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSF
 EKKTGSGDAE AKNAVNIQID NGGQPVDLGY NITGYKQGA GSSYLSWQEG NWSLVVRASN
 INGESPDDLA KNVNILEQE TLPAPNTVQ ITLNVAGTTD YNRNSVVWQA GTVVVSVHFF
 DPIQAVKMAT SM

EF047-3 (SEQ ID NO:175)

ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAAGTGCAG CGACAACCTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCACT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTCTTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCGAA TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-4 (SEQ ID NO:176)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGB KSTENTDSRS SAAESTTVES TKASATKESE
 SKATTKSSDA KPSGTTTADS KATASSTKEA ANNSSAEMQS PAKNANPEDQ ANQVLNQLAN
 MFPGQGLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSF
 EKKTYGSDAE AKNAVNQIID NGGQPVLDGY NITGYKQGAA GSSYLSWQEG NWSLVVRASN
 INGESPDDLA KVVVNILEQE TLPAPNTVGQ ITLNVAGTTD YNRNSVVWQA GTVVYSVHHF
 DPIQAVKMAT SM

EF048-1 (SEQ ID NO:177)

TAAGGAGAAA AGTTCATGAA AAAAAGAAAAG GTTTTATTTA CAGCAGTTAT GGTATTGGCA
 GGATTACAGT TGCTAAGTGG TTGCGGCAAA ACAGAAACCTT CGGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATTG AATATTTTCC AGATGGTCAA
 TTAGGAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTTGC CATTCCGTAT
 ATTTTTGATA ATGAAAAACA TTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACCGCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGTCTATGGT GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA
 AAAACGGTCT TTAAGAAGC GGTGAAGAA GAAAAGAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTGCCA GTTGGCGGAC
 TAA

EF048-2 (SEQ ID NO:178)

MKKRKV LFTAVMVLG LQLLSGCGKT EASANDTVVL RYAYASNSQP VIDSMMKKFGE
 LVEEKTGKV QIEYFPDQQL GGETELIELT QTGAIDFAKV SGSALESFSK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYYDSGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTKERL TAKQEQAIEE AAKESTAFEK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLQPLHES FKNSEHGEL YQAIRQLAD

EF048-3 (SEQ ID NO:179)

TTGCGGCAAA ACAGAAGCTT CGGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATTG AATATTTTCC AGATGGTCAA
 TTAGGAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTTGC CATTCCGTAT
 ATTTTTGATA ATGAAAAACA TTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACCGCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGTCTATGGT GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAACGGTCT TTAAGAAGC GGTTGAAGAA GAAAAGAAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTGCGCA GTTGGCGGAC
 TAA

EF048-4 (SEQ ID NO:180)

CGKT EASANDTVVL RYAYASNSQP VIDSMKKFGE
 LVEEKTGDKV QIEYFPDQQL GGETELIELT QTGAIDFAKV SGSALESFSK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYDSDGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTERL TAKQEQAIEE AAKESTAF EK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLVLPLHES FKNSSSEHGEL YQAIRQLAD

EF049-1 (SEQ ID NO:181)

TGAGACTCTT TCTTTTTCAG AATGAGGTAT GGTATAGTTA TAACAGANAT AAAACTANAA
 AAAACAGGAG TGCATAAGAG AATGAAGAAA AAATAATCT TAGCTGCAGC GGGCGCAATG
 GCCGTTTTTA GTTTAGCAGC GTGTTCAAGC GGTTCAAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA
 AAACAAAGAG CAGCCTATGA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AGATGAAGAC
 TTAATAACAG CTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
 TCAGAAGATG ATGCCAAAGC TGTCAGAAA GAAATCACTG ACGGCGGCGA TTTTCAAAAA
 ATTGCTAAAG AAAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
 GATTCAACAAG CAACAACCTGT TCCTGCCGAA GTTAAAGAAG CTGCCTTCAA ATTAAAGAT
 GGCGAAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
 GTAGTAAAA TGACGAAAA CAAAGCAAAA GGCAATGACA TGAAACCTTA TGAAAAAGAG
 ATCAAGAAAA TTGCTGAAGA AACAAAATTA GCCGATCAAA CATTTGTTTC GAAAGTCATT
 AGTGACGAAT TAAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
 GCAGGCTACA TGCAAACTGA ATCTTCAAGC GCTTCTTCA AGAAAAAGA ATCAAAATCA
 AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
 AGCAAAACAA CAGAATCTTC TTCTAAATAA

EF049-2 (SEQ ID NO:182)

MKKK LILAAAGAMA VFSLAACSSG SKDIATMKGS
 TITVDDFYNQ IKEQSTSQQA FSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
 FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEEL KTAWASFHPE VEAQIIQVAS
 EDDAKAVKKE ITDGGDFTKI AKEKSTDTAT KKDGGKIKFD SQATTVP AEV KEAAFKLKDG
 EVSEPIAATN MQTYQTTYV VKMTKNKAKG NDMKPYEKEI KKIAEETKLA DQTFVSKVIS
 DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
 KTTESSEK

EF049-3 (SEQ ID NO:183)

GTGTTCAAGC GGTTCAAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

AAACAAAGAG CAGCCTATSA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AATGAAGAC
TTAAAAACAG CTTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
TCABAAGATG ATGCCAAAGC TGTCAAGAAA GAAATCACTG ACGGCGGCGA TTTCACAAAA
ATTBCTAAAG AAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
GATTCACAAG CAACAACCTST TCCTGCCGAA GTTAAAGAA3 CTGCCTTCAA ATTTAAAGAT
GGCBAAGTGT CAGAACCAAT TCCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
GTATGTGAAA TGACGAAAAA CAAAGCAAAA GGCATGACA TGAAACCTTA T3AAAAAGAG
ATCAAGAAAA TTGCTGAAGA AACAAAATTA GCGCATCAAA CATTTGTTTC GAAAGTCATT
AGTGACGAAT TAAAAGCGGC CAATGTGAAA ATTAAGATG ATGCCTTCAA GAACGCTTTA
GCAGGCTACA TGCAAACTSA ATCTTCAAGC GCTTCTTCAG AGAAAAAGA ATCAAAATCA
AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
AGCAAAACAA CAGAATCTTC TTCTAAATAA

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EF049-4 (SEQ ID NO:184)

CSSG SKDIATMKGS

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TITVDDFYNQ IKEQSTSQQA PSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEDL KTAWASFHPE VEAQIIQVAS
EDDAKAVKKE ITDGGDFTKI AKEKSTDAT KKGKGIKIFD SQATTVPAAV KEAFAFLKDG
EVSEPIAATN MQTYQTTYVY VKMTKNKAKG NDMKPYEKEI KKIAEETKLA DQTFVSKVIS
DELKAANVKI KDDAFKNALA GYMQTESSSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
KTTESSSK

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EF050-1 (SEQ ID NO:185)

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TAGGGTCTGG AAAAGCAGTC AACTGACTTC TTTTCCAAGC CCTTTTTTATG TTCATCGCAG
AAAGGATGNA AAAAAATGAA CATGCCCAAA AATATCNGIT ATTTTCTTTT GCTAATGGGT
CTTGTTCTAT TATTAAGTGC TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAAACA CACCAACGCT TTTTTTTTAT
GGTTACGCAG GAACTAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGGA GAAACAAGGT
GCCACAACCTC AAGAATTAGT CCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAAG TTCTATTTGA AGATAATAAA
AACAATGAAT GGAATCAAAC AGAATGGATA AAAAACACAT TACTCTATTT ACAAAAAAAT
TATCAAGTGA ACAAAGCCAA TATTGTCGGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAAAT CGTCAGCATT
GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACCGAACTA
GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTTGGATT ATCAAGAGAT GATTAATGTT
GTTCCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
GATGGAACGG TGCCGTTATC TAGTGCCCTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

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EF050-2 (SEQ ID NO:186)

MNMPKN IXYFSLMGL VLLSACQIG ATTKDDNQAA

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TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLlyLQKNY QVNKANIVGH SMGGVSLGRY
LGTYGQDTSI PKIEKFVSIQ APFNDPIDTS QQQTIELE NGPTEKSSRY LDYQEMINNV
PEKLPILLIG GQLSPTDLSG GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQHLHEN
PEVDQLLIEF LWPSKK

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EF050-3 (SEQ ID NO:187)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
 GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAACAA CACCAACGCT TTTTTTTCAT
 GGTACGCAG GAACTAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGGA GAAACAAGGT
 GCCACAACCTC AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
 GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAG TTCTATTTGA AGATAATAAA
 AACAATGAAT GGAATCAAAC AGAATGGATA AAAAACACAT TACTCTATTT ACAAAAAAAT
 TATCAAGTGA ACAAAGCCAA TATTGTCTGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
 TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAATT CGTCAGCATT
 GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACGGAACCTA
 GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTGTGATT ATCAAGAGAT GATTAATGTT
 GTTCCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
 GATGGAACGG TGCCGTTATC TAGTGCCCTTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
 ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
 AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

EF050-4 (SEQ ID NO:188)

CQIG ATTKDDNQAA

TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
 ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLLYLQKNY QVNKANIVGH SMGGVSGRLRY
 LGTYGQDTSI PKIEKFVSIG APFNDFIDTS QQQTIELE NGPTEKSSRY LDYQEMINVV
 PEKLPILLIG GQLSPTDLSD GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQLEHN
 PEVDQLLIEF LWPSKK

EF051-1 (SEQ ID NO:189)

TAAAAGAAAA GAGGCGTTCA AATGTCTAAA CAAAAAAGG CTGTGTTCCCT GCTTAGTTTA
 TTCAGTTTAG TTGCCCTAAT TGCTGCATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
 ACAAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG
 AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAAGTGG AACCTATGAT
 AGTTCTGGAA AATTACAGAT GCAAATTGAA AAAGGCCTAA AAGCCGATGT ATTTTCTCTCA
 GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGGAAAACCA GCTCGTTCTT ATTGTGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTAAA AAAAGCCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGCTC AATATGCCGA AGAAGGCTTA AAAGCTTTAG GCGCTTGCTC TTATGTAGAA
 AAACACGCAA GCTTTGGCAC GAATGTAACA GAAGTCCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGGCAGAGAT GCAGCAACCA ATTCAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATT TTTTACAGAG TCAACAATGC
 AGAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-2 (SEQ ID NO:190)

MSKQ KKAVFLLSLF SLVALIACT NQPQKETVST KKEEITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGTYDS SGKLQMIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
 PLENQLVLI VPNQDQAKWH DFSDLKKAQM IAIGDPASVP ACQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIPVGVKVA
 SKKQKSADAF LNFLSQQCR KYFXNIGFKL TK

EF051-3 (SEQ ID NO:191)

ATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
 ACAAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAAGTGG AACCTATGAT
 AGTTCTGSA AATTADAGAT GCAAATTGAA AAABSCCTAA AAGGCGATGT ATTTTCTCA
 GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGGAAAACCA GCTCGTTCTT ATTBIGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTAAA AAAABSCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGGTC AATATGCCGA AGAABGCTTA AAABCTTAG GCGCTTGGTC TTATGTAGAA
 AAACACGCAA GCTTGGGCAC GAATGTAACA GAATGCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGCGACAGAT GCACCAACCA ATTCAAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATT TTTTACAGAG TCAACAATGC
 AGAAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-4 (SEQ ID NO:192)

CT NCPQKETVST KKEBITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGYDS SGKLQMQIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
 PLEENQLVLI VPNQDQAKWH DSELKKAQM IAIGDPASVP AGQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIPVGVKVA
 SKKQKSADAF LNFLQSQQCR KYFXNIGFKL TK

EF052-1 (SEQ ID NO:193)

TAAAGTAGGA GAAGCGCAAG CGAAAAAAGT GAATCAATCG GCAGCGTATC AAGTAGTGAT
 CCCACAAATGG GTACCATGGG TAGCATTATC TTTGACAGTA GCACTTGCTG GATTGATTGC
 TTACTTAGTT CGTCGTGGAG AGAAGTGGA AAACGAAGGG GAAGTGACAT AATGAGANGA
 NGAAATCTTC NGTTTTTATT ATTGTTGGTT CTATTAATTT ATATTCCTCA AACAACTTAT
 GCAGAAAATA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAAACTTC AGACATACCA
 TCAAAAAAAA ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGATTA CCTAAAACTG GTGACAATCG AATAACTTGG
 CTAAGCTGGT TTGGCATATT GTTTTAAATA AGTAGTTTTT GGCTGTTTCT ATTTAGACAA
 TTATGTAGAA AAGGAGAATA A

EF052-2 (SEQ ID NO:194)

MRXX
 NLXFLLLLVL LIYIPQTTYA ENRETTEVGI GFTKTSIPS KKNPVNVLP QTTIQSLSIV
 RSRTQIKRLP KTGDNRIWL SWFGILFLIS SFWLFLRQL CRKGE

EF052-3 (SEQ ID NO:195)

AGAAAAATA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAACTTC AGACATACCA
 TCAAAAAAAA ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGAT

EF052-4 (SEQ ID NO:196)

ENRETTEVGI GFTKTSIPS KKNPVNVLP QTTIQSLSIV
 RSRTQIKR

EF053-1 (SEQ ID NO:197)

TAGTCATGGC ACCATAACAA GGAGGAGAGA AGTGAGATGA AAAAATACCT TTTGCTTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGTTTTTTAG GTCTTTTCAG CTTCTGTCAT TCAGACACTG CGTTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGATTACC AGCGACAGGT
 ACCACCAATC AAGCACCATT TATTTATTTG GGAATCAGCC TTATCACTAT AGGCATATTA
 TTTATTAAAA GGAGAAGAGA AGATGAAAAA AACAGTATTA GCAGTAGTAG GGATTGTAGG
 ATTTAG

EF053-2 (SEQ ID NO:198)

MKKYLLLSL FLGLFSFCHS DTAFGEAAEY NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGRLPATGT TNQAPFIYLG ISLITIGILF
 IKRRREDEKN SISSSRDCRI

EF053-3 (SEQ ID NO:199)

TTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGA

EF053-4 (SEQ ID NO:200)

FGEEAAEY NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGR

EF054-1 (SEQ ID NO:201)

TAAATAAAAA ATTATTTGGA GGAAATTACA ATGAAAAAAA TTATTTTATC AAGCTTGTTT
 AGTGCACTAC TAGTATTCGG TGGCGGAAGT ATAACAGCAT TCGCTGACGA TTTAGGACCA
 ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCGCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAACCG AGCCTACAAC ACCGAGTGAG CCAGAAAAGC CAACAGAACC AACAACGCCA
 ATTGATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTACTCCAGA ACAACCGAAA
 GAACCAACTC AACCAGTGAT TCCAGAAAAA CCAGCAGAAC CAGAAACACC AAAAACTCCT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA GTGGAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTGAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACAGAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAGGAT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAGCAA GTGATGGAAA AATGAAAGTA
 TTGCCACATA CAGGAGAGAA ATTCACTCTC CTTTCTCTCTG TATTGGGAAG CTTCTTTGTA
 TTAATTTTCTG GATTCTTTTT CTTTAAAAAG AATAAGAAAA AAGCTTAA

EF054-2 (SEQ ID NO:202)

M KKIILSSLFS AVLVFGGGSI TAFADDLGPT DPATPPITEP TDSSEPTNPT
 EPVDPAEPPV IPTDPTEPSK PTEPTTPSEP EKPTPTPI DPGTPVEPTE PSEPTEPSQP
 TEPTTPSEPE KPVTPPEQKE PTQPIVEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 QSAGTQPSIP IETSNLAEVT HVPSETTPI T EAGEEIVAV DKGVP LTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKVL PHTGEKFTLL FSVLGSFFVL ISGFFFFKKN KKKA

EF054-3 (SEQ ID NO:203)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

A

ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCBCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAAACG AGCCTACAAC ACCGAGTBAG CCAGAAAAGC CAACAGAACC AACCAACGCCA
 ATTSATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTAATCCAGA ACAACCGAAA
 GAACCAACTC AACCAAGTAT TCCAGAAAAA CCAGCABAAC CAGAAACACC AAAAATCCTT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA CTGCAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTBAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACABAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAAGAT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAACAA GTGATGGAAA AATGAAAGTA
 T

EF054-4 (SEQ ID NO:204)

DDLGP DPATPPITEP TDSSEPTNPT
 EPVDPAEPPV IPTDPTEPSK PTEPTTPSEP EKPTEFTPI DPGTPVEPTE PSEPTEPSQP
 TEPTTPSEPE KPVTPPEPK PTQPIPEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 CSAGTQPSIP IETSNLAEVT HVPSETTPI T EAGEEIVAV DKGVPLTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKV

EF055-1 (SEQ ID NO:205)

TAACAAAAGG TTGTTTTGTC TTTCTTGTGT AAAAGGGCAA GAAAGGCTAG CGAGTTAAAA
 GGAGGTTTTT CAATGAAAAA AAAGCGTTAT TTAATGATTG TGTGTCTACT ATCTTCTCCT
 AGTTTTTTTA TAAATGTTGA AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGGTCCTCCG CAAGGAGATC AACGAAGTGG TGGTTCGACA
 CAGACCACCA CAACTGGCTC AACGCTCCCT CGTACAGGGA GCAAGAGTCA GGCAAATTTG
 AGCATTCTCN GNTTCGCCTT AATCGGTTTG CCGGGAATCG TACATAGAAA GAAGGGACGA
 CATGAAGCAA ACTAA

EF055-2 (SEQ ID NO:206)

MKKKRYL MIVCLLSSPS FFINVEASDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGSTLPR TGSKSQANLS
 ILXFALIGLA GIVHRKKGRH EAN

EF055-3 (SEQ ID NO:207)

AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGGTCCTCCG CAAGGAGATC AACGAAGTGG TGGTTCGACA
 CAGACCACCA CAACTGGCTC AACG

EF055-4 (SEQ ID NO:208)

SDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGST

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF056-1 (SEQ ID NO:209)

TAAATGAAAA AAAAGCGTTA TTTAATAATT GCGTGTTCAC TATTTTCCCC TAGTTTTTTT
ATAAATGTTG AAGCATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAAT
CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TCGGGATCCC
AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGT3 GTGGTTCGAC ACAGACCACC
ACAGCTGGCT CGCAGCTCCC TCGTACAGGA AGCAAGAGTC AGGCAAACCT GAGCATTCTT
GGTCTTGTCT TGATTGGTCT TGTCGGAATG GTCCAGAGAA AGAAGGGACG ACATGAAGCA
AACTAA

EF056-2 (SEQ ID NO:210)

MKKKRYLIIA CLLFSPFFI NVEASEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
EPAGPLQGDQ RSGGSTQTTT AGSQLPRTGS KSQLNLSILG LVLIGLVGMV QRKKGRHEAN

EF056-3 (SEQ ID NO:211)

ATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAAT
CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TCGGGATCCC
AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
ACAGCTGGCT CGCAG

EF056-4 (SEQ ID NO:212)

SEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
EPAGPLQGDQ RSGGSTQTTT AGSQ

EF057-1 (SEQ ID NO:213)

TAATGTTTAT TGGCTGGGCC AGTCAATGTT GAAAATGGGG AAGGAGGAAT TCAGATGAAA
ATCATAAAAA GGTTTAGTTT GGTATGTTTA GGGCTATTGA TCATTGGGTT GCNAACAAAA
AGCGNTATGG CTGAAGAAAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT TACCTAAAAC AGGCGAGTCT
GAAAATCCGC TGTATTCCTT GATAGGAGTT AGTTTGTGG GGATAGTCAT TTATTTAATT
AATAAAATGA AACGAGAGAA GGAGTTTATT TAA

EF057-2 (SEQ ID NO:214)

MKI IKRFLVCLG LLIIGLXTKS XMAEENNYES NGQASFYGTY
VYENEKESND VAYTQQSEEQ GRNNLAASGQ AVLPKTGESE NPLYSLIGVS LLGIVIIYLN
KMKREKEFI

EF057-3 (SEQ ID NO:215)

AAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT

EF057-4 (SEQ ID NO:216)

EENNYES NGQASFYGTY
VYENEKESND VAYTQQSEEQ GRNNLAASGQ AV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF058-1 (SEQ ID NO:217)

TGAAGAACGT TCTATTTGGT TGACGATTGC AGGCCTGCTA ATCATTGGGA TGGTAGTCAT
 TTGGCTATTT TATCAAAAAC AAAAAAGAGG AGAGAGAAAA TGAAGCAATT AAAAAAGTTT
 TGGTACACCG TTAGTACCTT GTTACTAATT TTGCCACTTT TCACAAGTGT ATTAGGGACA
 ACAACTGCAT TTGCAGAAGA AAATGGGGAG AGC3CACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC SATGCAATG GGAATGTCAC TGTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCACTTT ACGAAATGAT CAAGCAAACA
 SATGGTTCCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCATATTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAATTTGGC GAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAT TAACAGTTAA AAATCTTGAG GTTGGTTTCT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAATT AATTGAAAAT CAAACAAAAA CACCATTAC AATTGAAGCA
 AACAATCAAA CACCTGTTGA AAAACAGTC AAAAATGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTC CATTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTAAAT CCAGCGTATA TTCTACGCT AACACCAGGC
 GGCACACTAA AATTTCGTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCAATGTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGGCGG GAGCTTCCTT TGTGCTCCGT GATCAAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCAGAGGC TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AAACACAAAG GTACCTTACC TTCAACAGGT GGCAAAGGAA TCTACGTTTA CTTAGGAAGT
 GGCGCAGTCT TGCTACTTAT TGCAGGAGTC TACTTTGCTA GACGTAGAAA AGAAAAATGCT
 TAA

EF058-2 (SEQ ID NO:218)

MKQLKKVW YTVSTLLLL PLFTSVLGTT
 TAFAEENGES AQLVIHKKKM TDLDPPLIQN SGKEMSEFDK YQGLADVTF IYNTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGTDD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAATNMVAVF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVISKS EGSPGTVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENGT
 GELTVKNLEV GSYILEEVKA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDVAI GEKIKYQISV NIPLGIADKE GDANKYVKFN LVDKHDAAIT FDNVTSGEYA
 YALYDGDVI APENYQVTEQ ANGFTVAVNP AYIPTLTGPG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGKRFIK VDGDTVATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFVY
 NEQSYGTEN LVSPEKVPNK HKGTLPTSTG KGIYVYLGSG AVLLLIAGVY FARRRKENA

EF058-3 (SEQ ID NO:219)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGAAGA AAATGGGGAG AGCGCACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC GATGCAATG GGAATGTCAC TGTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCACTTT ACGAAATGAT CAAGCAAACA
 GATGGTTTCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCAATTTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAAATTGGC GAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAAT TAACAGTTAA AAATCTTGAG GTTGGTTCGT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAATT AATTGAAAAT CAAACAAAAA CACCATTTAC AATTGAAGCA
 AACAATCAAA CACCTGTTGA AAAAACAGTC AAAAATGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTC CATTTGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTTAAT CCAGCGTATA TTCTACGCT AACACCAGGC
 GGCACACTAA AATTCGTTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCAACTGTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGGCGG GAGCTTCCTT TGTCGTCCGT GATCAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGCG TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AACACAAAG GTACCTTACC T

EF058-4 (SEQ ID NO:220)

EENGES AQLVIHKKKM TDLDP LIQN SGKEMSEFDK YQGLADVTF S IYNVTNEFY E
 QRAAGASVDA AKQAVQSLTP GKPVAQGT TD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAAATNMVAF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVSKS EGPSTVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENG T
 GELTVKNLEV GSYILEEVKA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDVAI GEKIYQISV NIPLGIADKE GDANKYVKFN LVDKHDAA LT FDNVTSGEYA
 YALYDGDVI APENYQVTEQ ANGFTVAVNP AYIPTLTPGG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VDGDTVATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFVV
 NEQSYGTEN LVSPEKVPNK HKGT

EF059-1 (SEQ ID NO:221)

TAGATTGGAA GAATGAAAAT GAAAAAATG ATTATTATTG CCTTATTCAG TACAAGCCTT
 TTAGCAGGGG GAAGCAGTGT TTCTGCTTAT GCGCAAGAAT CAGAAGGAAA TCTTGGTGAA
 ACAACAGGGA GTGTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTA CCAGAAAAAC CAGTAGAACC AAATAAACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCGAGCCAG AAAAGCCTGT GGCAGTTGTT CCTSAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGST GGTAAAGCCA AATGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT T3AAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGCTGA T3GATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGCAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTACTTCC TTACTCTGGT
 GAAAAAATGG GCATAATTGG GTCAATCGST GGTGTATGTT T3ACTGTTTT ATCAGGAATC
 TTAATTTATA AAAAACGTAA AGTGTAG

EF059-2 (SEQ ID NO:222)

MKKMI IIALFSTSL AGGSSVSAYA QSEGNLGET T3SVLPDEPN VPTDPITPSE
 PEQPTSTPT EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTPSV
 PEQPTSPVP EKPVEPNKPT EPEKVPVVP EKPVPQQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPIETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKVLPYTGE KMGIGSIAG VCLTVLSSIL IYKKRKV

EF059-3 (SEQ ID NO:223)

AGAAGGAAA TCTTGCTGAA
 ACAACAGGGA GTGTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTG CCAGAAAAAC CAGTAGAACC AAATAAACCA
 ACCGAGCCAG AAAAGCCTGT GCCAGTTGTT CCTSAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGGT GGTAAAGCCA AATGGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGCTGA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGCAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTAC

EF059-4 (SEQ ID NO:224)

EGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTSTPT EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTPSV
 PEQPTSPVP EKPVEPNKPT EPEKVPVVP EKPVPQQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPIETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKV

EF060-1 (SEQ ID NO:225)

TGAAAAATAG ACAAGGAGCA CGCGATGATG ACAATGAAAA GTAAAGGGTC ACTTCTGGTG
 ACGTTGGGAA TACTTTTAAAC CGTTGGCATT GCGAGTCTAA TTGTTTCTTC TGAGAGTTTT
 GCAGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
 AAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCACTCA CTGATAAAGA TAAAAAACG
 TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
 CAGACGTCAT TACCAAGGAC AGGTGAACGA AATAGCACGT GGCTTTACAG CCTTGGTATT
 GCCTGTTTAC TCGTAGTACT AACAAGTTTC TATTATTGTA ATAAAAAAG GAAAAAGGAA
 AAATAA

EF060-2 (SEQ ID NO:226)

MMT MKSKGSLVLT LGILLTVGIA SLIVSSESFA EEVGQTNIGV TFYGGKEPLK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TSLPRTGERN STWLYSLGIA
CLLVVLTsfY YLNKKRRKKEK

EF060-3 (SEQ ID NO:227)

AGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
AAAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCAGTCA CTGATAAAGA TAAAAAACG
TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
CAGACGTCAT

EF060-4 (SEQ ID NO:228)

EEVGQTNIGV TFYGGKEPLK
TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TS

EF061-1 (SEQ ID NO:229)

TAATGGAACG ACCGACAGAA GAAGATTTTG AACTTACAAA TTAATAATTAA AATGGAGGAA
ATAATGATGA AAAAAATTCT TTTTGCTAGT TTATTAGTG CCACACTACT ATTTGGGGGA
AGTGAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCCAT
GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
GAAAAAATCT TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
CCAAGCAAGC CAATCGACGT TGTGTAAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
CCTAGTGTAA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAGAAAAA
GGTGTTCAC TTACACAAAC AGCAGAAGGG TTAAACCTA TTCAATCNAG TTACAAAGTA
TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TTTACCATAC
ACAGGTGAAG AAATGAATAT CTTTTTATCT GCCGTAGCGG TATCTTGCTCT GTAG

EF061-2 (SEQ ID NO:230)

MMKILFASL FSATLLFGGS EISAFQEI PDDTTTPPIE
VPTPESTPEK PTDPTPIEP PVDPVEPPIT PTEPTEPTEP TTPTEPTTPT EPSEPEQPTE
PSKPVEPEKP VTPSKPAEPE KVTPTPKPTE SEKPVQPAEP SKPIDVVVTP TGELNHAGNG
TQQPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVEKG VPLTQTAEGL KPIQSSYKVL
PSGNVEVKGK DGKMKVLPYT GEEMNIFLSA VAVSCL

EF061-3 (SEQ ID NO:231)

GAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCCAT
GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
GAAAAAATCT TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
CCAAGCAAGC CAATCGACGT TGTGTAAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
CCTAGTGTAA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAGAAAAA
GGTGTTCAC TTACACAAAC AGCAGAAGGG TTAAACCTA TTCAATCNAG TTACAAAGTA
TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF061-4 (SEQ ID NO:232)

QEII PDDTTTPPIE

VPTERTPEK PTDPTPIEP PVDPEPPIT PTEPTPTPT TTEPTTPT EPSEPEQPT
 PSKPVEPEK VTPSKPAEPE KTVPTKPTF SEKPVFAEP SKFIDVVVTP TGELNHAGNG
 TQOPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVKES VPLTQTAEGL KPIQSSYKVL
 PSGNVEVKKG DGKMKV

EF062-1 (SEQ ID NO:233)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 DACTGGGTAA CTGTCCCTAT TTTTTTTCTA AGTGTCTTA GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA TAACGACGGT TCAACCCCAAT
 AACCCCGACC TGCACTCAGA AAAGGAAACA CCTAAACGGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG AACTACTTTC TCAACCGACC AAAGTAGAAB AAGTAGCGCC AGAAAATAAA
 GGTACTGAAC AAAGTTCAGC TACCCCAAAT SATACACAA ACCCGCAACA ACCAACAGTA
 GGAGCTGAAA AATCAGCACA AGAACAACCA TAGTAAGCC CTGAAACAAC CAATGAACCT
 CTAGGGCAGC CAACAGAAGT TGCACCAGCT GAAAATGAAB TGAATAAATC AACGTCCATT
 CCTAAAGAAT TTGAAACACC ABACGTTGAT AAAGCAGTTS ATGAAGTAAA AAAAGATCCA
 AACATTACCG TTGTGAAAA ACCAGCAGAA SACTTAGGCA ACGTTTCTTC TAAAGATTTA
 GCTGCAAAAG AAAAAGAACT AGACCAACTA CAAAAAGAAC AAGCGAAAAA GATTGCCCAA
 CAAGCAGCTG AATTAAAGC CAAAAATGAA AAAATTGCCA AAGAAAATGC AGAAATTGCG
 GCAAAAAACA AAGCNGAAAA AGAGCGNTAN GANAAAGAA TCGCNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTT CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTCGTTCG ATTAAAGGCG GAAAATTTAT CAAAGCAACT
 GATTTTAAATA AAGTAAATGC AAGGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT
 ATGGGNGGGA AAGNTACTGG CAACTTCCAG AATTCCTTTG TAAAAGAGGC AAATCTTGGG
 TCTAATGGTG GGTATGCGGT TCTTTTAGAA AAAAAATAAC CAGTGACAGT GACCTATACA
 GGACTAAACG CTAGTTATTT AGGACGTAAA ATTACAAAAG CAGAATTTGT TTATGAACCTA
 CAATCCTCAC CAAGCCAAAG TGGAAAGTTA AATGCAGTAT TTCAAACGA TCCGATTATC
 ACNGCTTTTA TTGGTACAAA CAGAGTCAAT GGTAAAGATG TTAACACAG CTTAACGATT
 AAGTTCTTTG ATGCGTCAGG TAAAGAAAGTA CTACCAGATA AAGATAGTCC ATTTGCGTAT
 GCGCTGTCTT CTTTAAATTC AAGTTTAAAC AATAAAGGTG GCCATGCGGA ATTTGTTTCT
 GATTTTGGGG CNAACAATGC GTTCAAATAC ATTAATGGNT CNTATGTGAA AAAACAAGCG
 GATGGAAAAAT TTTACTCACG GGAAGATATT GACTATGGCA CAGGACCTTC TGGATTGAAA
 AATAGTGATT GGGACGCTGT AGGTCAACAAG AATGCCTACT TTGGTTCAGG TGTAGGTCTA
 GCNAATGGNC GTATTTCTCT TCTTTTGGT ATGACAACAA AAGGAAAAAG TAATGTGCCT
 GTATCTAGTG CGCAATGGTT TGCCTTTAGN ACTAACTTAA ATGCGCAATC AGTGAAGCCT
 ATTTTCAATT ATGGGAATCC AAAAGAACCA GAAAAAGCAA CGATTGAATT CAATNGATAC
 AAAGCCAATG TCGTTCCTGT NCTTGTCN NATAAAGAAG TCACTGATGG NCAGAAAAAT
 NTCAATGATT TAAATGTGAA NCGTGGCGAT TCTTTACAAT ACATTGTGAC AGGGGATACG
 ACAGAAGTTG CCAAAGTAGA TCCAAAAACA GTAACNAAAC AAGGGATTCC AGATACNTTT
 GATGCAGAAA AAGTGACGAT TGATTTATCC AAAGTGAAAG TTTATCAAGC AGACGCAAGT
 CTNAACGANA AAGACTNAAA AGCTGTTGCT GCAGCNATTA ATTCAGGAAN AGCTAAAGAC
 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAAACCG TCACAGCAAT GATGAAAACC
 AACGCNGACG GNTCNGTTGT TTTAGCAATG GGGTATAAAT ATTTACTTGT CTTGCCGTTT
 GTAGTGAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGNN
 GAAACGGTAA CAAATACAGT GATTAACCAT GTGCCAGGTA GTAATCCTTC CAAAGATGTA
 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTCTCTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAATCT TCCGAACGTC CAGCNAACTA TGGCGGAATN
 ACNGAAGAAT GGGGCATGAA TGATGTCCTG GACACGACCC ATGATCGTTT CACAGGNAAA
 TGGCACGCTA TTACNAANTA TGACCTTAAA GTAGGGGANA AAACGTTAAA AGCAGGAACA
 GATATTTCTG CCTACATTCT TTTAGAAAAC AAAGACAATA AAGACTTGAC GTTTACNATG
 AATCAAGCAT TATTGGCNGC NTTAAATGAA GGAAGCAATA AAGTAGGCAA ACAAGCTTGG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCTGTGTATC TGGAAGTCGA ACGGATNAAA ACAGGTGAGG TAGAAAAACAC GCAAACAGAA
 AACTACAACA AAGAGCTTGT NCGTTCTAAT ACNGTGTGTA CGCATAACNC TGATGATCCA
 AAACCAACCA AAGCCGTTC AACAAGAAA GGGGAAGANA TTAANCATGG AAAAGTNGCT
 CGTGGTGATG TTCTTTCTTA TGAAATGACN TGGGACTTAA AAGSGTACGA TAAAGACTTT
 GCCTTTGATA CAGTCGATCT TGCGACAGGC GTTCTTTCT TCGATGATTA CGATGAAACG
 AANGTGACAC CAATCAAAGA CTTACTTCGT GTCAAAGATT CTAAAGGGGN AGACATTACG
 AACCAGTTCA CGATCTCNTG GGACGATGCC AAAGGCAGGG TGACNATNTC TGCCAAAGAC
 CCACAAGCCT TTATTCTAGC GNATGGTGGG CAAGAATTGC GTGTAAACNT CCTTACAAAA
 GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTCAGGGG AACAAAATAC ATTGTGNCNA
 CGAATTAAAA CCAATACNGT TGTCAACCAT ATTCCAAAAG TGAANCCTAA AAAAGACGTG
 GTTATTAAAG TNGGTGACAA ACAAAGTCAA AATGGNBTCA CAATCAAATT AGGGGAGAN
 TTCTTCTATG AAGTTACAAG TAGTGACATT CCTGCAGAAAT ACGCTGGNGT TGTGGAAGAA
 TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGCCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAA GGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTNGATG CGATGAATCT AAAAGAAAAC AAAACSTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TAAAAACNAA TACGGTAGTG ACNCATAGGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAG CGCAAGCACC AGTAGAGCCA
 TTAGTGCTAG AAAAGGCAAG TGTNGTGCCA GAATTGCTGC AAACAGGCGA AAAACAAAAT
 GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTB GCTTAGCAGG CTTAGCCTTT
 AAACGTAGAA AAGAAACAAA ATAA

EF062-2 (SEQ ID NO:234)

MKAKK QYKTYKAKNH WVTVPILFLS VLGAVGLATD NVQAAELETTQ PETTTVQPNN
 PDLQSEKETP KTAVSEEATV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEQPV VSPETTNEPL GQPTVEVAPAE NEVNKSTPIP KEFETPDVVK AVDEVKKDPN
 ITVVKEPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAEKAKNEK IAKENAEIAA
 KNKAERKEXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DFTKLRKDM GSKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSQSQSGTLN AVFSNDEPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
 GKFPSPEDID YGTGPSGLKN SDWDVAVGHKN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXT NLNAQSVKPI FNYGNPKPE KATIEFINXK ANVVPVLVFN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDTFD AEFVTIDLSK VKVYQADASL
 NXKDXKAVAA AINSGXAKDV TASYXLNLDQ NVTAMETN ADGSVVLAMG YKYLVLPLFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGFH HAITYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGFVAR GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKGXICTN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGBR IFNTNTVNHV PKVXPVKDVV
 IKVGDQKQSN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGGDDIS KLEFMTFEQG VVKITASQAF XDMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIESEFNN EKIKTNTVVT HTPEKPTTP EKTIVVPPTP KTPQAPVEPL
 VVEKASVVPE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RKKETK

EF062-3 (SEQ ID NO:235)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 CACTGGGTAA CTGTCCCTAT TCTTTTCTTA AGTGTGTTAG GAGCGTAGG ATTAGCTACT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GATAATGTAC	AAGCCGCGGA	ATTAGATACG	CAACCAGAAA	CAACGACGGT	TCAACCCAAT
AACCCCGACC	TGCAGTCAGA	AAAGGAAACA	CCTAAAAGCG	CAGTATCTGA	AGAAGCAACA
GTACAAAAAG	ACACTACTTC	TCAACCGACC	AAASTABAAG	AASTAGCGCG	AGAAAAATAA
GGTACTGAAC	AAAGTTCCAG	TACGCCAAAT	GATACCAGAA	ACGTCGAACA	ACCAACAGTA
GGAGCTGAAA	AATCAGCACA	AGAACAACCA	GTASTAAGCG	CTGAAACAA	CAATGAACCT
GTAGGGCAGC	CAACAGAAAGT	TGCACCAGCT	GAAAATGAA	TGAATAAATC	AACGTCCATT
CCTAAGAAT	TTGAAACACC	AGACGTTGAT	AAAGCAGTT	ATGAAGTAA	AAAAGATCCA
AACATTACCG	TTGTTGAAAA	ACCAGCAGAA	GACTTAGGCA	ACGTTCTCTC	TAAAGATTTA
GCTGCAAAAG	AAAAAGAAGT	AGACCAACTA	CAAAAAAAT	AAGCGAAAAA	GATTGCCCAA
CAAGCAGCTG	AATTAAGAAGC	CAAAAAATGAA	AAAATTGCA	AABAAAATGC	AGAAATTGCG
CAAAAAAACA	AAGCNGAAAA	AGAGCGNTAN	GAAAAAATA	TGBCNGAATA	CAACAAGCAT
AAGAACGAAA	ACAGCTATGT	CAATGAAGCG	ATTAGTAAAA	ACCTAGTGTT	CGATCAATCT
STCGTGACGA	AAGACACTAA	AATTTCTGTC	ATTAAAGGCG	GAAAATTTAT	CAAAGCAACT
GATTTTAATA	AAGTAAATGC	AGGGGATTCA	AAAGATATCT	TTACAAAAAT	ACGGAAAGAT
ATGGGNGGGA	AAGNTACTGG	CAACTTCCAG	AATTCCTTTC	TAAAAGAGGC	AAATCTTGGG
TCTAATGGTG	GCTATGCGGT	TCTTTTAGAA	AAAAATAAA	CAGTGACAGT	GACCTATACA
GGACTAAACG	CTAGTTATTT	AGGACGTAAA	ATTACAAAA	CABAATTTGT	TTATGACTCA
CAATCCTCAC	CAAGCCAAAG	TGGAACGTTA	AATGCAATAT	TTTCAACGA	TCCGATTATC
ACNGCTTTTA	TTGGTACAAA	CAGAGTCAAT	GGTAAGGATG	TTAAAAACAG	CTTAACGATT
AAGTTCTTTG	ATGCGTCAGG	TAAAGAAGTA	CTACCABATA	AAGATAGTCC	ATTTGCGTAT
GCGCTGTCTT	CTTTAAATTC	AAGTTTAACG	AATAAABSTG	GCCATGCGGA	ATTTGTTTCT
GATTTTGGGG	CNAACAATGC	GTTCAAATAC	ATTAATBENT	CNTATGTGAA	AAAACAAGCG
GATGGAATA	TTTACTCACC	GGAAGATATT	GACTATGGA	CAGGACCTTC	TGGATTGAAA
AATAGTGATT	GGGACGCTGT	AGGTCACAAG	AATGCCTACT	TTGTTTCAGG	TGTAGGTCTA
GCNAATGGNC	GTATTTCCCTT	TTCTTTTGGT	ATGACAAAA	AAGBAAAAAG	TAATGTGCCT
GTATCTAGTG	CGCAATGGTT	TGCCTTTAGN	ACTAATTTAA	ATGTCGAATC	AGTGAAGCCT
ATTTTCAATT	ATGGGAATCC	AAAAGAACCA	GAAAAAGCAA	CGATTGAATT	CAATNGATAC
AAAGCCAATG	TGCTTCCTGT	NCTGTGCCN	AATAAAGAA	TCACTGATGG	NCAGAAAAAT
NTCAATGATT	TAAATGTGAA	NCGTGGCGAT	TCTTTAGAA	ACATTGTGAC	AGGGGATACG
ACAGAACTTG	CCAAAGTAGA	TCCAAAAACA	GTAACNAAA	AAGGGATTCC	AGATACNTTT
GATGCAGAAA	AAGTGACGAT	TGATTTATCC	AAAGTGAAAG	TTTATCAAGC	AGACGCAAGT
CTNAACGANA	AAGACTNAAA	AGCTGTTGCT	GCAGCNATTA	ATTCAGGAAN	AGCTAAAGAC
GTGACTGCTT	CTTATGANCT	CAATTTAGAT	CAAAACACCG	TCACAGCAAT	GATGAAAACC
AACGCNGACG	GNTCNGTTGT	TTTAGCAATG	GGGTATTAAT	ATTTACTTGT	CTTGCCGTTT
GTAGTGAAAA	ATGTAGAAGG	CGATTTTGAA	AATACAGCTG	TTCAGCTGAC	AAANGATGNN
GAAACCGTAA	CAAAATACAGT	GATTAACCAT	GTGCCAGGTA	GTAATCCTTC	CAAAGATGTA
AAAGCAGATA	AAAACGGTAC	AGTTGGCAGT	GTTTCTCTAC	ATGATAAAGA	TATTCCGTTA
CAAACAAAAA	TTTATTATGA	AGTGAAATCT	TCCGAACCTC	CAGCNAACTA	TGGCGGAATN
ACNGAAGAAT	GGGGCATGAA	TGATGTCTTG	GACACGACCC	ATGATCGTTT	CACAGGNAAA
TGGCACGCTA	TTACNAANTA	TGACCTTAAA	GTAGGGGANA	AAACGTTAAA	AGCAGGAACA
GATATTTCTG	CCTACATTCT	TTTAGAAAAC	AAAGACAATA	AAGACTTGAC	GTTTACNATG
AATCAAGCAT	TATTGGCNGC	NTTAAATGAA	GGAAGCAATA	AATAGGCAA	ACAAGCTTGG
TCTGTGTATC	TGGAAGTCGA	ACGGATNAAA	ACAGGTGACG	TAGAAAAACAC	GCAAAACAGAA
AACTACAACA	AAGAGCTTGT	NCGTTCTAAT	ACNGTGCTGA	CGCATACNCC	TGATGATCCA
AAACCAACCA	AAGCCGTTCA	TAACAAGAAA	GGGGAAGANA	TTAANCATGG	AAAAGTNGCT
CGTGGTGATG	TTCTTTCTTA	TGAAATGACN	TGGGACTTAA	AAGGGTACGA	TAAAGACTTT
GCCTTTGATA	CAGTCGATCT	TGCGACAGGC	GTTTCTTTCT	TGATGATTA	CGATGAAACG
AANGTGACAC	CAATCAAAGA	CTTACTTCGT	GTCAAAGATT	CTAAAGGGGN	AGACATTACG
AACCAGTTCA	CGATCTCNTG	GGACGATGCC	AAAGGCACCG	TGACNATNTC	TGCCAAAGAC
CCACAAGCCT	TTATTCTAGC	GNATGGTGGG	CAAGAATTGG	GTGTAACNCT	CCCTACAAAA
GTCAAAGCCG	ATGTTTCTGG	NGATGTTTAT	AATTCAGCGG	AADAAAAATAC	ATTTGGNCAA
CGAATTAAAA	CCAATACNGT	TGTCAACCAT	ATTCCAAAAG	TGAANCCTAA	AAAAGACGTG
GTTATTAAAG	TNGGTGACAA	ACAAAGTCAA	AATGGNGGCA	CAATCAAATT	AGGGGAGAA
TCTTCTATG	AATTTACAAG	TAGTGACATT	CCTGCAGAA	ACGCTGGNGT	TGTGGAAGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGGCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAG TGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTITNGATG CGATGAATCT AAAAGAAAAC AAAAACGTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TTAAAAACNA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAAAC CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TG

EF062-4 (SEQ ID NO:236)

AELDTQ PETTTVPNN
 PDLQSEKETP KTAVSEETV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
 AEKSAQEOPV VSPETTNEPL GQPTVEVAPAE NEVNKSTSIP KEFETPDVVK AVDEVKKDPN
 ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
 KNKAERKXX KEVAEYNKHK NENSYVNEAI SKNLVFIQSV VTKDTKISSI KGGKFIKATD
 FNKVNAGDSK DIFTKLKRDG GGGXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAFFVYELQ SSPSQSGTLN AVFSNDFIIT AFICTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGAINNAFKYI NGSYVKKQAD
 GKFYSPEDID YGTGSPGLKN SDWDVGHKN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXST LNNAQSVKPI FNYGNPKEPE KATIEFIKXX ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGITRFTD AEKVTIDLSK VKVYQADASL
 NXKDXKAVAA AINSXAKDV TASYXLNLDQ NTVTAMKTH ADGSVVLAMG YKYLVLVLPFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSFDFE ADKNGTVGSV SLHDKDIPLO
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGFVAF GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLRLV KDSKGXELTH QFTISWDDAK GTVTXSADDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQE IKTNITVNNHI PKVXPKKDVV
 IKVGDKQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISKDLVKH DKFSGQWSVF
 ANSNFVLADG TKNVKGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVVPPTP KTPQAPVEPL
 VVEKASV

EF063-1 (SEQ ID NO:237)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 CACTGGGTAA CTGTCCCTAT TCTTTTTCTA AGTGTGTAG GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA CAACGACGGT TCAACCCAAT
 AACCCCGACC TGCAGTCAGA AAAGGAAACA CCTAAAACGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG AACTACTTTC TCAACCGACC AAAGTAGAAG AAGTAGCGCC AGAAAAATAA
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 GATTTTAATA AAGTAAATGC AGGGGATTCA AAAGATATCT TTACAAAATT ACGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF063-3 (SEQ ID NO:239)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF063-4 (SEQ ID NO:240)

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EF064-1 (SEQ ID NO:241)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF064-2 (SEQ ID NO:242)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. naccalis* Genes.

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EF064-3 (SEQ ID NO:243)

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 TTTTNGATG CGATGAATCT AAAAGAAAAA AAAACGTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAAAT CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TTA AACNAA TACGGTAGTG ACNCATACCG CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAD CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TGTNGTGCCA GAATTGCGGC AAACACGCGA AAAACAAAAT
 GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTB GCTTAGCAGG CTTAGGCTTT
 AAACGTAGAA AAGAAACAAA ATAA

EF064-4 (SEQ ID NO:244)

VTIDLSK VKVYQADASL
 NXKDXKAVAA AINSXKXADV TASYXLNLDQ NTVTAMMKTN ADGSM/LAMG YKYLVLVLPFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTSKW HAITYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS WYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDLVSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKSGXDIIN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFQQR IKTNITVNNHI PKVXPBKDVV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IKVGDQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNGGDDIS KLFTMTFEQG VVKITASQAF XIAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EMTVIVPPTP KTPQAPVEPL
 VVEKASV

EF065-1 (SEQ ID NO:245)

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 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CCGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
 TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
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 AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
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 ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTAGATGG TTAATTGCAT
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 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTTCGGTAAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
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 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
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TABLE 1 Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAACCTAAAC AACCGGTAAA ACGGAAAAAA CGGTGACGCT ATACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA ATAAAGGAAA TTGATTTTACC AATGACTAAT
 ACAACASTAA ATCCACTTTA CATGATCGCA GGTTTAATTA TCGTTATAGT GGTATTAGC
 TTTTCCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF065-2 (SEQ ID NO:246)

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 LKALDITYNQ THGELTNRKT YFLLVTDGVA NTELDGYLEH TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLN SNISYFDFYK TEVGPFFVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTIDAAT LVSSTMTNQG TIAKEFPEAT
 IPHNENAHAC DVTPEPTIT KDIENTEHLN LTNREDSFDW HVTAFGNET STWTQASMVD
 DINKVLDIID VEVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSG HTYTMITITK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSENKP VTPPPVDPNI AKDVEGQEH
 DLNTRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIIT DVEVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYLS GHTYTMITIT KIKASATDDE LAPYIEQGGI PNQADLNFGN
 EGDVLHSENKP TVTPPAPTPE DPTITKDIEG QEHLDLTNRD QEFKWNVKT FGNSTSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTKNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDLVH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFKGSAS KGIHLPMNTN TVNPLYMIAG LIVLIVAISF
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EF065-3 (SEQ ID NO:247)

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 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GGGGTAGTTT TTCAGATAAT
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 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTCAATAGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAAGG TAAAAACAGC TTTCCGTAAC
GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
ACTGATGTAA AAGTCACAGA TGAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACANCAAG CAGACAGCTA TGACTATTTA
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GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAAGG AAGCCGACTT GAACCTTGGC
AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
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GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
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CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGG CAGAAGACCC AAAAAACCT
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EF065-4 (SEQ ID NO:248)

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DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTPEMIX QADSVDYLSG HTYMTITTK
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DLTNRDQEFK WNVKTAFGNE TSTWTQASMD DDINKVLDIT DVKVTDENGK DVTANGKVTQ
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EF066-1 (SEQ ID NO:249)

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ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTAGCTGCAT
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TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAATTACTA ACCAAGGSTA TGAATGATT AATCGGTATT GGGAAAGTST TGAATCTTTA
 AGTTGAGTGA ATTCATACTT TGATAAATAT AAAACAGAAAG TGGGTCCTTT TGTAAAACAA
 GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
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 GCTTCATTAA CATTGCGCAA TCAATTBTAT ATTCAATCTG CGACCGCTAD GACGATGCT
 GGAAATGATG TGCCTGTTCA AATTACCGA CAAATCATT CAGCAACTAG TACAGAAGGT
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 TGGCATGTCA AAACAGCCTT TGCAACGAA ACCASTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACCA AAATGGTAAA
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 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF066-2 (SEQ ID NO:250)

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 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD FLAQSTPATA SLTIANQFDI QSATATDDAG
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 DLTNRDQEFK WNVKTAFCNE TSTWTQASMV DDINKVLDT DVKVTDENGK DVTANGKVTQ
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 EGDVLHNSKP TVTPAPTPE DPTITKDIEG QEHLDTNDR QEFKWNVKT FGNSTSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PKQPLPKPKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
GITKNKKRKN

EF066-3 (SEQ ID NO:251)

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GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCTGATGG AAAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
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EF066-4 (SEQ ID NO:252)

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LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHVEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
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EF067-1 (SEQ ID NO:253)

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AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
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ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAGACCAATA CCAATGATTC AATCAATBAA TATCCAGATC CAAGACATCC TCTTCAAGTC
 TCAGTGGAAAT ATAGTAATGA CTACCAAGST GCAGCAJGAG AAGTTTTAGC GTTAAACCAA
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 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCAAGG CAGCATGGTG
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 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDHYK TEVGPFFVKQE
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 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMHQG TIAKEFPEAT
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 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSG HTYTMITTK
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 DLTNRDQEFH WNVKTAFGNE TSTWTQASMV DDINKVLDT DVKVTDENGK DVTANGKVTQ
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 EGDVLHNSKP TVTPPAPTPE DPTITKDIEG QEHLDTNRD QEFKWNKTA FNETSTWTQ

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
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EF067-3 (SEQ ID NO:255)

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 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAAATT AAATGGAACG TCAAAACAGC TTTTCGGTAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAAT GTTAGACATC
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 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TT

EF067-4 (SEQ ID NO:256)

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 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFCKSAS KGIH

EF068-1 (SEQ ID NO:257)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 ATTACCACTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT
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 ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGSTAA CGAAACAATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTTACTTTTT	TGACTGCCGT	TTTGAATGCA	GCCAATGATT	TAACCAATGT	GATTACTCAA
ATTACCAAGT	GGGCGTTAGG	GAATTTAACT	GGTGTGATA	TTGATTTGAC	GGAAGTGAAT
CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
GAAACGTTAG	CAGCTGACGG	CTCATACATT	AGTGCACCGA	TTAGTGATGG	TTTAGGGTTA
GTTTTAGCCC	AAAATGTTTC	AAACATCTTA	CAAGATTTGA	ATGCGGCAGT	TCAAGCTTTG
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TTACCAACTA	CCGTTTCAAC	ACCTCAAAAT	TTATCCAATA	ATTTAGATGC	TCGTTTGTGA
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GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGGC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

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ACTGTGCTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA
GTGGACTTAG CDACACCAAC CATTCATTCT ATTACCGGAA ATTCTABTAA AGGTACGAA
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EF068-2 (SEQ ID NO:258)

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FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADEA TVTAPTITGV TGNSTAGYEV
KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGAVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
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PATATTPADV TAPTVDNITG HSGSGYEITG TADPNTTIEV RDP3GAVIGT GTSDANGDFT
VTLPTGTTNP GDTLTVIGKD MAGNESQPT3 VLVPADATVT APTVTGVTGN SVAGYQVTGT
ADPNATIEIR DADGNVIATG TADGTG3FAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
LASGKATAKQ TVNVVAKNDT GLE3QPTTAM TPADVTTPTI GDITGDS3TG YEITGTADPN
TTIEVRNPDG TIIGTTTDD QGNFTVDLPA GAANPGD3LT VVGKDG3NE SQPTEVT3PE
DATVAAPT3T TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTT3GA GAFTITLPTG
TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITG3TNG YQVVGAAEVG
TTVEVRDADG TVLGMATTGT D3KYTVTLEP GKASANETIT VVAKNAT3KE SQPATATPTV
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FYN3SEQLLA SGN3TTGGTF SVHIAAGLAT EKETLTALIT DTQGNV3PKT TFMT3ADITG
EPEIKIAAPT V3SVLGT3KA GYLIK3TAEP NRIQ3ISNRL LRSVIAVGAT DAEGNFAIQL
TAGQATAQ3S L3LATATDGAG H3YSTATTFMT PADPTNPGGG NGNTGGN3GN TGGNTGN3GA
TGGNNGN3SN TGSNPN3GSG L3TTG3GL3S LGNGLG3NGS GYH3KL3TIS YGTGNH3GKTG
YLPSTGEKES SAVT3SLFGA FVALLAS3MI IKRKRKN

```

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF068-3 (SEQ ID NO:259)

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 GCGGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
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 GTAACAGGTA ATTCACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
 GTTGAAATCC GAAATGCAGG AGGCACCGTA ATAGGCACAG GTACCGCTGA TGGGACAGGA
 GCGTTTACAG TTACCGTTCC CGCAGGTGAA GCAGGCGCCA ATGAAACGTT AACC GCCGTA
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 CCAACAACGT TCCAAACACC AGCGGATGAA GCAACCGTAA CCGCACCAAC AATCACAGGA
 GTGACAGGTA ATTCACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
 GTTGAGATCC GAAATGCAGG AGGTGCCGTG ATAGGTACAG GTACTGCTGA TGGGACAGGG
 GCATTTACAG TTACCATTTCC CGCAGGTGAA GCAGGTGCGA ATGAAACGTT AACC GCCGTA
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EF068-4 (SEQ ID NO:260)

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 TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAV SGALPLLAAG
 GSGVNELVDA SLLGTTTFTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTEXTP TTFQTP

EF069-1 (SEQ ID NO:261)

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 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
 CTATTATCAA ATGTTACGTC AAATAATGAC AGTGGCACTT CAACGAGTAA TCGTTGGACA
 GCGGCAAAAC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
 AATGTAGCTG CAGCAGGCAG CGCAGCAATC AATACCAATG TCACGATTGA TCTTTCAAAA
 GTTACTTTTT TGACTGCCGT TTTGAATGCA GCCAATGATT TAACCAATGT GATTACTCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATTACCAGT3 GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTCAC GGAAGTGAAT
 CGTCAATTG3 AATTAGTTAA TAACATTGAA AACTTABGTG CTGCTTCATT TACAGCTCCG
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 GTTTTAGCC3 AAAATGTTTC AAACATCTTA CAASATTTGA ATGCGGATGT TCAAGCTTTG
 GAGGCAAAA3 GTACCAGTAT CCAAGTAAT CTTGTGCGCG CAGCTATAAA TGCAGCCTTG
 CTTCTGTGCA AABGACCGGT AAACGTGGCT GTTTCAGGTG CTTTGCCTTT ATTAGCGGTT
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 TTACCAACTA CC3TTTCAAC ACCTCAAAAT TTATCCAATA ATTTAGATBB TCGTTTTGTA
 GGAACAGTCG TTCAAACAGA TCTTTTAGAC GTTAATTTAT TAGCAACABD AGACGGTGTA
 TCCAACATTT ATTTTGCTGC AGGCCTACT AGTGAAGTAA CCGCACCAAC AATCACAGGA
 GTAACAGGTA ATTCAACAGC AGGTACGAA GTTAAAGGAA CTGCCGATBC CAATGCCACG
 GTTGAAATCC GAAATGCAGG AGGCACCGTA ATAGGCACAG GTACCGGTSA TGGGACAGGA
 GCGTTTACAG TTACCGTTCC CGCAGGTGAA GCAGGCGCCA ATGAAACGTT AACC GCCGTGTA
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 GTTAAAGGAA CTGCCGATGC CAATGCCACG GTTGAAATCC GAAATGTABG AGGCACCGTA
 ATAGGCACAG GTACCGCTGA TGGGACAGGA GCGTTTACAG TTACCGTTCC CGCAGGTGAA
 GCAGGTGCCA ATGAAACGTT AACC GCCGTGTA GCGAAAAACG CCAGCGGNAC AGAAAGTACG
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 GCGAAAAACG CCAGCGGTAC AGAAAGTACG CCAACAACGT TCCAAACACC AGCGGATCCT
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 GTCCTTGGTA CTGCAACAAC TGGAACTGAC GGAATATATA CAGTGACTTT AGATTACAGGA
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 CAACCAGCAA CCGCGACAAC ACCAGCTGAT GTCACCTGCAC CAACAGTGA TAACATCACA
 GGCAACTCTG GTTCGGGTTA TGAATTTACA GGAACAGCAC ACCCTAATAC AACAATCGAA
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 TTCCAAACAC CAGCAGATGA AGTAGTGGCA CCGCCAAGTG TCGACAAAGT TACTGGGAAT
 ACAACACAAG GATATCAAGT GACAGGTACC GCTGAACTTG GCACCACTAT TGAAGTTCGT
 GCAACAGACG GAACAGTTTT AGGCACCGCA ACAACTGGAC CGACTGGGCA ATATACTGTG
 ACGTTAGCTT CAGGAAAAGC AACAGCTAAA CAAACAGTGA ATGTAGTTGC TAAAAATGAT
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 ATTGGTGACA TTACTGGAGA TTCAACAAC TGGTTATGAAA TCACTGGGAC GCGGACCCCT
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 GAAGATGCAA CCGTAGCAGC ACCAACTGTG ACGACTGTTA CAGGAACAAC TGCCACTGGG
 TATCAAGTAA CCGGCACGGC AGAGCCAAAT GTCACCATTT AGATTCAAAA TGAAGCAGGT
 TTAGTTATTG CTACGGGAAC GACTGATGGT GCTGGCGCAT TTACAATAC TCTTCCGACG
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 AGTAATCCGA CTGCTTTCAA AACACCTGCT GATCCAGATG CACCACTGC GACACCTACT
 GTTGACAAAA TCACTGGTAG CACGACAAAC GGCTATCAAG TAGTAGGAGC AGCAGAAGTT
 GGTACAACAG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGCG AACTACTGGA
 ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
 ACTGTCTGTA CGAAAAATGC AACAGSAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTCGACTTAG CCACACCAAC CATTGATTCT ATTACCGGAA ATTCTAGTAA AGGTTACGAA
 ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCAAA CGGAACCATC
 ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGACTCTAAG AGCTGGCGTA
 GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAAGTCAA
 CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACTAT TACGAAGGTT
 GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAACTG CTGATCCAAA TGTCACGGTT
 CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGCCA ATACAACCTA TGGAGGTACC
 TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAE CGCACTAACC
 ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAAG CGATATTACG
 GGAGAACCAG AGATTAATAAT TCGGGCACCA ACTGTTTCTT CAGTTTATAG AACGTCTAAA
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 CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
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 GGACATTACA GTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
 GGCAATGGTA ACACTGGCGG AAATAACGGC AATACAGGCG GCAATACAGG AAACAATGGC
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 GGCTACTTAC CTAGCACAGG TGAAAAAGAG TCTTCAGCCG TGACAACAAG TTTGTTTGCG
 GCCTTTGTCT CACTCCTTGC GAGCATGGGA ATCATCAAAC GCAAACGTAA AAACCTAG

EF069-2 (SEQ ID NO:262)

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 TSGALGNLTG VDIIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAY SGALPLLAVG
 GSGVNELVDA SLLGTTTIVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLIV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTEXTT TTFQTPADEA TVTAPTITGV TGNSTAGYEV
 KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
 TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
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 PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGAVIST GTSDANGDFT
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 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKDGDSNE SQPTEVTVPE
 DATVAAPTIV TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTEDSA GAFTITLPTG
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 TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
 TGGNNGNSN TGSNPNGGSG LGTTGSGGLS LGNGLGTNGS GYHPKLTIS YGTGNHGKGT
 YLPSTGEKES SAVTSLFGLA FVALLASMI IKRKRKN

EF069-3 (SEQ ID NO:263)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GUGAAAACCG CCAGCGGTAC AGAAAGTACC CCAACAACCT TCCAAACGCG ACGGGATCCT
 AATACGCCCG TGCGGACGCG AATTGTTGAG ACTGTAACAG GTAGTACAA AAAAGGCTAT
 GAGGTCAAAG GGAAGTCTGA AATTGGGACC ACCATTGAGG TTGCGGATGC AGCTGGCAGC
 GTCTTTGGTA CTGCAACAAC TGGAACTGAC GAAAAATATA CAGTGASTTT AGATTTCAGGA
 ACAGCAATAG CAAATCAAAC GGTGAGCGTT CTAGCGAAAA ACCGCTAGTG CACGGAAAGT
 CAACCAGCAA CGGCGACAAC ACCAGCTGAT CTCACTGCAC CAACAGTTGA TAACATCACA
 GCAACTCTG GTTCGGGTTA TBAATTTACA GBAACAGCAG ACCCTAACGC AACAATCGAA
 GTTCGTATC CATCTGGGGT AATCATTGCT ACAGGTATCT CTGATGCBAA TGGTGATTTT
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 GCGACTGCCG ATGCGACTGG TTCTTTGCT GTGAACCTTC CAGCTGCGAC GCAAAATGCG
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 ACAGTTGTTG GAAAAGACCG TGACGGCAAT GAAAGTCAAC CAACGGAAGT GACGGTCCCT
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EF069-4 (SEQ ID NO:264)

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 QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
 LASGKATAKQ TVNVVAKNDT GLESQPTTAM TPADVTTPTI GDITGDSTTG YEITGTADPN
 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKDGDCNE SQPTEVTVPE
 DATVAAPTIVT TVTGT

EF070-1 (SEQ ID NO:265)

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 CGCAAGATGC TTAATTTAGC AATATCAAGT GGTTTATTAT TTACGTGATT AGCAATCCCT
 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCAATCAG CAGCGGTCTT GGATATCGAA
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 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
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 GTTACTTTTT TGAAGTCCGT TTTGAATGCA GCCAATGATT TAACCAATGT GATTACTCAA
 ATTACCAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
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GTTTTAGCCC	AAAATGTTTC	AAACATCTTA	CAAGATTTGA	ATGCGGCAGT	TCAAGCTTTG
GAGGCAAAAG	GTACCAGTAT	CCCAAGTAAT	CTTGTCGCCG	CAGCTATAAA	TGCAGCCTTG
CTTCCTGTCA	AAGGCACGGT	AAACGTGGCT	GTTTCAGGTG	CTTTGCGCTT	ATTAGCGGTT
GGTGGTTCAG	GCGTAAATGA	GTTAGTGGAT	GCTTCTTTAC	TAGGCACAAC	CACGGTTACT
TTACCAACTA	CCGTTTCAAC	ACCTCAAAAT	TTATCCAATA	ATTTAGATGC	TCGTTTTGTA
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TCCAACATTT	ATTTTGCTGC	AGGCACACT	AGTGAAGTAA	CCGCACCAAC	AATCACAGGA
GTAACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAAATCC	GAAATGCAGG	AGGCACCGTA	ATAGGCACAG	GTACCGCTGA	TGGGACAGGA
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GCAACCGTAA	CCGCACCAAC	AATCACAGGA	GTGACAGGTA	ATTCAACGBC	AGGTTACGAA
GTTAAAGGAA	GTGCCGATGC	CAATGCCACG	GTTGAAATCC	GAAATGCAGG	AGGCACCGTA
ATAGGCACAG	GTACCGCTGA	TGGGACAGGA	GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA
GCAGGTGCCA	ATGAAACGTT	AACCGCCGTA	GCGAAAAACG	CCAGCGGCAC	AGAAAGTACG
CCAACAACGT	TCCAACACC	AGCGGATGAA	GCAACCGTAA	CCGCACCAAC	AATCACAGGA
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GTTGAGATCC	GAAATGCAGG	AGGTGCCGTG	ATAGGTACAG	GTACTGCTGA	TGGGACAGGG
GCATTTACAG	TTACCATTC	CGCAGGTGAA	GCAGGTGCGA	ATGAAACGTT	AACCGCCGTA
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GAGGTTCAAAG	GGACTGCTGA	AGTTGGCACC	ACCATTGAGG	TTCGCGATGC	AGCTGGCACG
GTCTTTGGTA	CTGCAACAAC	TGGAACGTGAC	GGAAAATATA	CAGTGACTTT	AGATTCAGGA
ACAGCAACAG	CAAATCAAAC	GCTGAGCGTT	GTAGCGAAAA	ACGCTAGTGG	CACGGAAAGT
CAACCAGCAA	CGGCGACAAC	ACCAGCTGAT	GTCACGTCAC	CAACAGTTGA	TAACATCACA
GGCAACTCTG	GTTTCGGGTTA	TGAAATTTACA	GGAACAGCAG	ACCCTAACAC	AACAATCGAA
GTTTCGTGATC	CATCTGGGGC	AGTCATTGGT	ACAGGTACCT	CTGATGCGAA	TGGTGATTTT
ACTGTAACGC	TACCAACGGG	AACGACCAAT	CCTGGGGATA	CGTTAACAGT	GATTGGAAAG
GATAACGCGG	GAAATGAAAG	TCAACCGACT	GAAGTCCTTG	TTCTGTGCTA	TGCCACGGTT
ACAGCACCAA	CTGTAACAGG	AGTAACAGGT	AATTACAGTTG	CTGGTTATCA	GGTGACAGGC
ACCGCTGATC	CGAATGCTAC	CATCGAAATT	CGTGATGCAG	ATGGGAACCT	GATTGCAACA
GGGACTGCCG	ATGGGACTGG	TTCTTTTGCT	GTGAACCTTC	CAGCTGGGAC	GGCAAATGCG
AATGAAACAT	TGACAGCGTT	AGCCAAAGAT	CCTGCTGGCA	ATACAAGTAC	ACCGACAACC
TTCCAAACAC	CAGCAGATGA	AGTAGTGGCA	CCGCCAAGTG	TCGACAAAGT	TACTGGGAAT
ACAACACAAG	GATATCAAGT	GACAGGTACC	GCTGAACCTG	GCACCACAT	TGAAGTTCGT
GCAACAGACG	GAACAGTTTT	AGGCACCGCA	ACAACCTGGAC	CGACTGGGCA	ATATACTGTG
ACGTTAGCTT	CAGGAAAAGC	AACAGCTAAA	CAAACAGTGA	ATGTAGTTGC	TAAAAATGAT
ACTGGACTTG	AGAGTCAACC	AACACAGCT	ATGACACCCG	CTGATGTTAC	CACACCAACA
ATTGGTGACA	TTACTGGAGA	TTCAACAAC	GCTTATGAAA	TCACTGGGAC	GGCGGACCCCT
AATACCACCA	TTGAAGTACG	GAACCCAGAT	GGAACAATTA	TTGGTACAC	GACAACGGAT
GATCAAGGAA	ACTTTACTGT	GGACCTTCCA	GCGGGAGCCG	CTAATCCTGG	TGATACATTA
ACAGTTGTTG	GAAAAGACGG	TGACGGCAAT	GAAAGTCAAC	CAACGGAAAT	GACGGTCCCT
GAAGATGCAA	CCGTAGCAGC	ACCAACTGTG	ACGACTGTTA	CAGGAACAAC	TGCCACTGGG
TATCAAGTAA	CCGGCACGGC	AGAGCCAAAT	GTCACCATTG	AGATTCAACA	TGAAGCAGGT
TTAGTTATTG	CTACGGGAAC	GACTGATGGT	GCTGGCGCAT	TTACAATCAC	TCTTCCGACG
GGCACAGCAA	CAGCTAACGA	AGCCTTAAC	GCCATTGCGA	AAGATGCTBC	TGGGAAAGAA
AGTAATCCGA	CTGCTTTCAA	AACACCTGCT	GATCCAGATG	CACCAAGTGC	GACACCTACT
GTTGACAAAA	TCACTGGTAG	CACGACAAAC	GGCTATCAAG	TAGTAGGABC	AGCAGAAGTT
GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGBC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA
ACTGTCTGTG	CGAAAAATGC	AACAGGAAAA	GAAAGTCAGC	CAGCTACAGC	AACTACACCA
GTCGACTTAG	CCACACCAAC	CATTGATTCT	ATTACCGGAA	ATTCTAGTAA	AGGTTACGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

ATCACTG3AA  CCGGGGAGCC  AAAAACCAGT  ATTGATGTCC  GTGACG3AA  TCGAACCATC
ATTGCTG3TA  CAACTGCTAA  C3AAACCGGC  CAATATADGG  TGACTCTAAT  AGCTGGCGTA
GTGACAC3AG  GAGAAACGAT  TACGATTATT  A3CAAAGATG  CGGCAG3TAA  TCGAAGTCAA
CCAG3TACAG  CCGTTATTCC  A3CGGATGTT  GTTTTAG3GG  CGCCAATTAT  TACGAAGGTT
GAAG3AAACA  AAG3CAAT3G  CTATACAGTC  ACTGGAAGTG  CTGATC3AA  T3TCACGGTT
CAATTTTACA  ATAGCAGTGA  ACAATTATTG  GTAAGTGGCA  ATACAATTAG  T33AGGTACC
TTCTCCCTTC  ATATTGCA3C  A3G3TTAGCA  A3AGAAAAAG  AAACGT3AA  C3CCTAACC
ACAGATACAC  AAG3AAAT3T  GAGTCTTAAA  A3CAGATTTA  TGACGCG3AG  C3ATATTACG
G3AGAACCCAG  AGATTAAAT  T3CGGCACCA  ACTGTTTCTT  CAGTTT3AG  AAGCTCTAAA
G3CGGCTACC  TCATCAA3G  AACAG3TGAA  C3AAAC3GAA  TCATTCAAT  TAGTAACCGA
CTATTAAGAA  GTGTGATT3C  T3TAG3TGCC  A3CGAT3CTG  AAGGCAACTT  C3CTATCCAA
TTAACAGCGG  GACAAGCGAC  T3CTCAACAA  A3TTTACTTG  CGACAG3TAA  C3ATGGCGCA
G3ACATTACA  GTACGGCTAC  AACCTTCATG  A3CCCA3CCG  ACCCAAG3AA  T3CTGGAGGA
G3CAATG3TA  ACATGGC3G  AAATAACGGC  AATACA3CG  GCAATADAG  AAACAATGGC
GCAACTGGCG  GGAATAAT3G  GAATG3TTCA  AACACA3GTT  CAAATC3AA  T3GAGGTTCT
G3TTTAG3CA  CAACAGGTTT  T3GCTTAGGT  T3ACTAG3CA  ATGGCCT3G  TACAAATGGT
A3TGGCTACC  ACC3TAAAT  AAGTACCATC  A3TTAT3GCA  CTGGAAT3A  C3GGAAAACA
G3CTACTTAC  CTAGCACAG  T3AAAAGAG  T3TTCA3CCG  TGACAACAAT  TTTGTTTGGC
GCCTTTGTCC  CACTCCTT3C  GAGCATGGGA  ATCATCAAAC  G3AAAC3TAA  AAAC TAG

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EF070-2 (SEQ ID NO:266)

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M KKKIVEDFNE FSQHKKWTKF FMLNLAISSG LLFTSLAIPV
SIAVTSGTIS ASAAVLDEL LSNVTSNNDS GTSTSNRWA ANQNQPVNFT VSGGALADAS
AVFSGQKQAV LVVPELRCN VAAAGSAAIN TNVTIELSKV TFLTAVLNAA NLTNVITQI
TSGALGNLTG VEDIDLTEVNR QLELVNNIEN L3AASFTAPE TLAADG3TIS AFISDGLGLV
LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAV SGALPLLAVG
GSGVNELVDA SLLGTTTTL FTTVSTPQNL SNNLDARFVG TVVQTDLLD NLLATADGVS
NIYFAAGTTS EVTAPTITGV TGNSTAGYEV K3TADANATV EIRNAGGTVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA FNASGTESTP TTFQTPADEA TVTAPTITGV TGNSTAGYEV
FGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA FNASGTESTP
TTFQTPADEA TVTAPTITGV TGNSTAGYEV K3TADANATV EIRNAGGTVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA FNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
VKGTAEVGTI IEVRDAAGTV LGTATTGTDG FYTVTLDSGT ATANQTL3V AKNASGTESQ
PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDP3GAVIGT GTSDANGDFT
VTLPTGTTNP GDTLTVIGKD NAGNESQPTV VLVPADATVT APTVTGVTGN SVAGYQVTGT
ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALANDP AGNTSTPTTF
QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
LASGKATAKQ TVNVVAKNDT GLE3QPTTAM TPADVTTPTI GDITGDSTT3 YEITGTADPN
TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGD3LT VVGKDG3GNE SQPT3TVPE
DATVAAPT3T TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTT3A GAFTITLPTG
TATANEALTA IAKDAAGKES NP3AFKTPAD PDAPVATPTV DKITG3TT3 YQVVGAAEVG
TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNAT3E SQPATATTPV
DLATPTIDSI TGNSSKGYEI T3TAEPKTTI D3RDADGTII AATTANET3Q YTVTL3AGVV
TPGETIT3IS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGY3T GTADPNVTVQ
FYN3SEQLLA SGNTTTGGTF SVHIAAGLAT EKETLTALT DTQGNV3PT TFMTPADITG
EPEIKIAAPT VSSVLGTSKA GYLIK3TAEP NRII3ISNRL LRSVIAVGAT DAEGNFAIQL
TAGQATAQQS LLATATDGAG H3STATTFMT PADPTNP3GG NGNTGGN3GN T3GNTGNNGA
TGGNNGNGSN TGSNPNG3G LGTTG3GLGS LGNGLG3NGS GYHPKL3TIS YGTGNHGK3G
YLPSTGEKES SAVTTS3LFGA FVALLAS3GI IKRKRKN

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EF070-3 (SEQ ID NO:267)

CGG TGACGGCAAT GAAAGTCAAC CAACGGAAGT GACGGTCCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAGATGCAA CCGTAGCAGC ACCAACTGTG ACGACTGTTA CAGGAACAAC TGCCACTGGG
 TATCAAGTAA CCGGCACGGC AGAGCCAAAT GTCACCATIG AGATTCACAA TGAAGCAGGT
 TTAGTTATTG CTACGGGAAC GACTGATGGT GCTGGCGCAT TTACAATCAG TCCTCCGACG
 GGCACAGCAA CAGCTAACGA AGCCTTAACT GCCATTGCGA AAGATGCTGC TGGGAAAGAA
 AGTAATCCGA CTGCTTTCAA AACACCTGCT GATCCAGATG CACCAGTCGC GACACCTACT
 GTTGACAAAA TCACTGGTAG CACGACAAAC GGCTATCAAG TAGTAGGAGC AGCAGAAGTT
 GGTACAACAG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGCG AACTACTGGA
 ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
 ACTGTCTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA
 GTCGACTTAG CCACACCAAC CATTGATTCT ATTACCGGAA ATTCTAGTAA AGGTTACGAA
 ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCABA CGGAACCATC
 ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGACTCTAGC AGCTGGCGTA
 GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAGTCAA
 CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACCTAT TACGAAGGTT
 GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAAGTG CTGATCCAAA TGTCACGGTT
 CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAACCTC TGGAGGTACC
 TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCACTAACC
 ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
 GGAGAACCAG AGATTAAAAT TGCGGCACCA ACTGTTTCTT CAGTTTATABA AACGTCTAAA
 GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
 CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
 TTAACAGCGG GACAAGCGAC TGCTCAACA AGTTTACTTG CGACAGCTAC CGATGGCGCA
 GGACATTACA GTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
 GGCAATGGTA ACACTGGCGG AAATAACGGC AATACAGGCG GCAATACAGG AAACAATGGC
 GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTCTT
 GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
 AGTGGCTACC ACCCTAAACT AAGTACCATC AGTTATGGCA CTGGAATCA CGGAAAAACA
 GGCTACT

EF70-4 (SEQ ID NO:268)

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DATVAAPTPT TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTDGA GAFTITLPTG
 TATANEALTA IAKDAAGKES NPFAFKTPAD PDAPVATPTV DKITGSTTHG YQVVGAAEVG
 TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
 DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETBQ YTVTLPAQV
 TPGETITIIIS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTTF GTADPNVTQ
 FYNSSQQLLA SGNNTTGGTF SVHIAAGLAT EKETLTALT DTQGNVSPKT TFMTPADITG
 EPEIKIAAPT VSSVLGTSKA CYLIKGTAEF NRIIQISNRL LRSVIAVGAT DAEGNFAIQL
 TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNEN TGGNTGNNGA
 TGGNNGNGSN TGSNPNNGSG LGTTGSGLGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKTG
 YL

EF071-1 (SEQ ID NO:269)

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 GTCCCGCCAT TTATCTGCAG GTTTAAGCCG TGGAAAGGGAA GTTATTTTBA CTTTCCTTTC
 ATGGCTTTTT TAAGAAAGGA GCATGCTATG TTTAAAAAAT TAATGATTCA ACTTGCTTTA
 GTGATTGGTT TAAGTTTAAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
 CCAATCAACT TTACTTATTT TCCCGGCTCT GCAAGCAATG AATTAATBET TTTACATGAA
 TCTGGAAACG AGCGGAACCT AGGACCACAC AGTTTAGACA ATGAAGTB3C CTATATGAAA
 CGAAATTGGT CAAATGCTTA TGCTCATAT TTTGTCGGAT CTGGTGGA3G AGTGAAACAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTAGCTCCTG CTGGCCAAAT TCAATATGGG GAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGCGACAT TTAATAAACA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTGGCTCAG AACATTGGTG CTGATTTTTC TCTGGACGAT
 GSAACA33TT ATGGCATACT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GGATTATTA AGCGCATTTG CACNAGATTT
 APAACG33CG TTTCNGNAAC AGGTGAGACT GGTCAATTAT CAGCCAGGTA A

EF071-2 (SEQ ID NO:270)

MF KKLMIQALV

IGLSLTIPMT AXAYTIEADP INFYFPGSA SNELIVLHES GNERNLGPHE LDNEVAYMKR
 NWSNAYVSYF VSGGGRVKQL APA3QIQYGA GSLANQKAYA QIELARTENA ATFKKDYAAY
 VNLRDLAQN IGADPSLDDG TGYGIVTHDW ITKNWWDHT DPYGYLARG LVKRIGTRFT
 TGVSTGETG HYSAR

EF071-3 (SEQ ID NO:271)

G TTTAAAAAAT TAATGATTCA ACTTGCTTTA

GTGATTGGTT TAAGTTTAAC GATTCCGATG ACGGCTTNGG CTTACACCAT CGAAGCGGAT
 CCAATCAACT TTACTTATTT TCCCGGCTCT GCAAGCAATG AATTAATTCT TTTACATGAA
 TCTGGAAACG AGCGGAACCT AGGACCACAC ACTTTAGACA ATGAAGTGGC CTATATGAAA
 CGAAATGGT CAAATGCTTA TGTCTCATAT TTTGTCGGAT CTGGTGGAGG AGTGAACAA
 TTAGCTCCTG CTGGCCAAAT TCAATATGGG GCAGGTTCTT TAGCTAATTA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGGCGACAT TTAATAAACA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTGGCTCAG AACATTGGTG CTGATTTTTC TCTGGACGAT
 GGAACAGGTT ATGGCATAGT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GGATTAGTAA AGCGCATTTG CACNAGATTT
 ACAACGGGCG TTTCNGNAAC AGGTGAGACT GGTCAATTAT CAGCCAGGT

EF071-4 (SEQ ID NO:272)

F KKLMIQALV

IGLSLTIPMT AXAYTIEADP INFYFPGSA SNELIVLHES GNERNLGPHE LDNEVAYMKR
 NWSNAYVSYF VSGGGRVKQL APAGQIQYGA GSLANQKAYA QIELARTENA ATFKKDYAAY
 VNLRDLAQN IGADPSLDDG TGYGIVTHDW ITKNWWDHT DPYGYLARG LVKRIGTRFT
 TGVSTGETG HYSAR

EF072-1 (SEQ ID NO:273)

TAATCAATGA AAAACGCACG TTGGTTAAGT ATTTGCGTCA TGCTACTGGC TCTTTTCGGG
 TTTTCACAGC AAGCATTAGC AGAGGCATCG CAAGCAAGCG TTCAAGTTAC GTTGACAAA
 TTATTGTTCC CTGATGGTCA ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTTAAATGAC GTCATTATC AAGTCTATGA TGTGACGGAT
 CCGTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACAGCG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACAGAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTCG TTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTC GATAAGGCGG ATACAACGTT GACACTTTTA
 CCACAATCAA TTGAGGTAAA AGTGGCTGGA AAAACAGTTA CTACAGGTTA CACTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAA CTTTGCAAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAC AGCAAACGGG
 TATCGTTGGC AAAAAGAAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT AATCAATAA

EF072-2 (SEQ ID NO:274)

MKNARWLSI CVMLLALFGF SQQALAEASQ ASVQVTLHLK LFPDQQLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDV FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAPEV VKEKASNLVV ILPVQDPQQQ SLTHIHLYPK
 NEENAYDLPP LEKTVLDKQQ GFNQGEHINY QLTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMLL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNNNSF YGGKKFLCNE
 RTTNSTVTCN Q

EF072-3 (SEQ ID NO:275)

ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTTAAATGAC GTCACCTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACASNG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACASAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTTA TTTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTCA GATAAGGCGG ATACAACSTT GACACTTTTA
 CCAGAATCAA TTGAGGTAA AGTGGCTGGA AAAACAGTTA CTACAGSTEA CACACTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAAA CTTTGCAAAAT
 CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAC AGCAAACGGG
 TATCGTTGGC AAAAAGAAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT A

EF072-4 (SEQ ID NO:276)

QLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDV FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAPEV VKEKASNLVV ILPVQDPQQQ SLTHIHLYPK
 NEENAYDLPP LEKTVLDKQQ GFNQGEHINY QLTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMLL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNNNSF YGGKKFLCNE
 RTTNSTVTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF073-1 (SEQ ID NO:277)

TAAATGAACA AATTAAATAC AAAATTACTG ATTGGCTATA TTCTTTTAAAG AGCCTTAATC
 ATTGCTGTGCT CTAGAGAATA TGGCTTCTTC GCTTTTSTGA TTCTGCTAGG CTTTTTAGTA
 TTGCTTCTCT ATCGAAAAAA GAAAAATGCC GCGACAAAA GCGATCAAAT GCCTTACTTA
 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAAA CAAATCATAC AATTGCAGCA AACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAAACA AACAAACGTA TGA AAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTA AAAAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA ATAA

EF073-2 (SEQ ID NO:278)

MNKLNTKLLI GYILLGALII AVAREYGFFA FVILVGFVLF VLYRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHELEIEQHEV KNKQTYENLE ESAQIIDQLS
 KLVKNDYEEI VSDDLDDLDV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF073-3 (SEQ ID NO:279)

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 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAAA CAAATCATAC AATTGCAGCA AACATGAAT
 GCTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAAACA AACAAACGTA TGA AAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTA AAAAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA AT

EF073-4 (SEQ ID NO:280)

YRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHELEIEQHEV KNKQTYENLE ESAQIIDQLS
 KLVKNDYEEI VSDDLDDLDV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF074-1 (SEQ ID NO:281)

TAAAGGAGTT CTCAAAAAT GAAGCTAAAA AAAATAATTC CTGCTTTTCC CTTTCTTTCA
 ACCGTTGCAG TTGCTTGTG GTTAACGCCT ACTCAAGCTT CTGCAGATGC TGCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTTG GTTGGATATT GGCATAASTG GGCCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTTCTA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACAG GATTCTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAATAGT
 CAAGGTCGCG CAGTTTATT GGCCTTGGT GGAGCAGATG CACATATTCA ATTAGTCAAA
 GCGGATGAAC AAGCCTTTGC GAATGAAATC ATTCTGCAAG TGGAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAAACA AACCGTCATC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCTATN ATATT

EF074-2 (SEQ ID NO:282)

MKLKK IIPAFPLLST VAVGLWLTPT QASADAADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTDATF RQEVAQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LYXI

EF074-3 (SEQ ID NO:283)

TGC TCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTG GTTGGATATT GGCATAACTG GGCCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTCTGA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACACG GATTCCCTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCGCG CAGTTTTATT GGCACCTGGT GGAGCAGATG CACATATTC AATTAGTCAAA
 GGCGATGAAC AAGCCTTTGC GAATGAAATC ATTCGTCAAG TGGAAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAACCA AACCGTCATC
 CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCT

EF074-4 (SEQ ID NO:284)

AADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTDATF RQEVAQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LY

EF075-1 (SEQ ID NO:285)

TAACCTATAA GAAAAAATC ACAACCTGTG ATAAATTATT GGAGGNAAAA TATGTCAAAA
 GGAAGAAAA TTTTGGCCAT TATCNTTGA ATTATCTTGG NTCTATTCT TGCAGTTGTT
 GGAATGGGAG CAAAACCTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
 GTAGAACGAT CTAAAAAAG TCAGGTCAAT TTAAACAATA AGGAGCCTTT TTCTGTTTTA
 TTATTAGGGA TTGATACAGG CGATGATGGG CGTGTGAGC AAGGTCGTTG GGATACAACA
 ATTGTTGCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TGCTCGCGAT
 ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAAGATAAAT TGAATCAGGC CTATGCTTTT
 GGTGGCGCAT CTTTAGCAAT GGACACAGTT GAAAACTATT TAAACATACC TATTAATCAT
 TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG CGGAATCGAA
 GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTTCA
 TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
 TACGGCCGCC AAGAACGTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAAA AGTCTTAAGT
 CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
 GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTGTC CTATCAACGT
GTGGATGAAC AAGAATTAAC TCGTGTCCAA CAAGAGTTGA AAAATCAATT GAATACAAA
TAA

EF075-2 (SEQ ID NO:286)

MSK KKFATIXGI IIXHFLAVVG MGAKLYWVVS KSMKTYETV
ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPREDQ TLVSLARDT
YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
NNNLTFSDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQREVI EGIVQKVLSL
NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSAPGKV KQDQLQGTGF MQDGVSYQRV
DEQELTRVQQ ELKNQLNTK

EF075-3 (SEQ ID NO:287)

ACTTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
GTAGAACGAT CTAAAAAAG TCAGGTCAAT TTAACAATA AGGAGGCTTT TTCTGTTTTA
TTATTAGGGA TTGATACAGG CGATGATGGG CGTSTCGAGC AAGGTGCTTC GBATACAACA
ATTGTGTCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TCGTCGCGAT
ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAABATAAAT TGAATCAAGC CTATGCTTTT
GGTGGCGCAT CTTTAGCAAT GSACACAGTT GAAAACTATT TAAACATACC TATTAATCAT
TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG GBAATCGAA
GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTTCA
TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
TACGGCCGCC AAGAACGTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAAA AGTCTTAAGT
CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA
GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTGTC CTATCAACGT
GTGGATGAAC AAGAATTAAC TCGTGTCCAA CAAGAGTTGA AAAATCAATT GAATACAAA

EF075-4 (SEQ ID NO:288)

KLYWDVS KSMKTYETV
ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPREDQ TLVSLARDT
YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
NNNLTFSDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQREVI EGIVQKVLSL
NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSAPGKV KQDQLQGTGF MQDGVSYQRV
DEQELTRVQQ ELKNQLNTK

EF076-1 (SEQ ID NO:289)

TAGAAAATAA CAGAGGAGCT GAAGGAAATG AAAGCATCAA CAAAAATTGG TATCGGTTTTA
AGCATTGCTG CAGTTGCAAG TGTCTCTGTT GCAGTCATCG CTTCTGAAAA AATTATTAAG
AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAAGT TTGTAGACGA TAAATTTGAT
GGAAACCAAA AATTATTATC GATTGTGAT GATTATCCG ATGATGAATT AGATTCTGTT
TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
GTTAAAGACA ATACAGATTC TTTAAAGAA CGCTTTTCA CATTATTGA AGATGCAATG
AAGTTAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATCTTT TSTTTCAACA
TAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF076-2 (SEQ ID NO:290)

MK ASTKIGIGLS IAAVASVSVA VIASEKIIKK VSHVSNRYKV KKFVDDDFDG
 NQKLLSIVDD LSDDELDVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNSFVST

EF076-3 (SEQ ID NO:291)

CATCG CTTCTGAAAA AATTATTAAG
 AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAACT TTGTAGACGA TAAATTTGAT
 GGAAACCAAA AATTATTATC GATTGTCGAT GATTATCCG ATGATCAATT AGATTCTGTT
 TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
 GTTAAAGACA ATACAGATTC TTAAAAGAA CGCTTTTCA CATTTCATGA AGATGCAATG
 AAGTTAAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATTCTT

EF076-4 (SEQ ID NO:292)

VIASEKIIKK VSHVSNRYKV KKFVDDKFDG
 NQKLLSIVDD LSDDELDVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNS

EF077-1 (SEQ ID NO:293)

TAATGTAAAG TGAATGATGG GAGAGAAAAA GAGATGAAGC ATGTAACAAA ATTGGGGATT
 ACAATTATAA CAGGAGTTTT GGCATTATTA TTTGAATTTA TTTTACATCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGGT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT GTTGACTGGT
 CGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGCTGAA GTCATTATG
 GATAACTCGC CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAAACCAG GGGAACTAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGGAC ATCAACAGTC GATGAATCTT CATTACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGG TGACGGCTCT
 TTGAAAATGG TTGCTGAAAA AACTGTAGCA GACAGTCAAT ATCAAACAAT TGTGAACCTA
 GTGAAAAGAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAGATCG CTATGCGGTA
 CCTTTTACAC TAGTTGCCCTA CCTAATTGCA GGTGTTGCTT GGTGTTGTTT CAAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCA
 ATTGCTTTAG TGGCAGGATG GGGTCGTTCA AGTCGTCATG GGGTCGTTAT TAAATCGGGA
 ACGATGGTCC AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAGAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAAACT GAAAAAATTG ATAAAACGAC TATTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG AACTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACCGA AGTACATGGG
 GAATGTTTTAC CACAAGATAA ATTAACATATT CTAAAAGAAT TGCTTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTAAA CTGCTBACGT TGTATTTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAABATAC CATGAAAATT
 GCCAAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATGTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCSTGGA CACTGTGTCA
 ATCTTATCTG CTGTGCGTGC TCGTCGAATT GGCCAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF077-2 (SEQ ID NO:294)

MKHVTKLGIT IITGVLLALF EFILHQPWNA YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSVE EINVGDENVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGEDELMSGSVNGDGS LKMAEKTVD SQYQTIIVNLV KESAAAPAHF VRLADRYAVP
 FTLVAYLIAG VAVFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMBESS RHGVVIKSGT
 MVEKLASAKT IAFDKTGTIT QGQLSVBQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
 VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTIESQETE KIDKTTIHIS
 RNTYLGRIT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVATIAA EVGITEVHGE
 CLPQDKLTIL KFLPKENHPV IMVGDGVNDA PSLAAADVGI AMGAGCATAA SETADVILK
 DDLSKVSQAV EIAQDTMKIA KQSVNLGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
 LSALRARRIG C

EF077-3 (SEQ ID NO:295)

TCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGCT TCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT CTGACTGGT
 GGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGGTGAA GTCATTATTG
 GATAAECTCG CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAAACCAG GGGAAATAGT TCCAGTTGAT
 GGCTTGCTAA AAACCGGAC ATCAACAGTC GATGAATCTT CATTACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGS TGACGGCTCT
 TTGAAAATGG TTGCTGAAAA AACTGTAGCA GACAGTCAAT ATCAAAACAT TGTGAACCTA
 GTGAAAGAAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAATCTC CTATGCGGTA
 CCTTTTACAC TAGTTGCCA CTAATTGCA GGTGTGCTT GGTTTTCTTC AAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGGAT GGGTCGTTCA AGTCGTCATG GGGTCCTTAT TAAATCGGGA
 ACGATGGTCG AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAAAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAACT GAAAAAATG ATAAAACGAC TATTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG ACAGTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACGCA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAACATT CTAAAAGAAT TGCTTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTGAAA CTGCTGCTGC TGTATTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAAGATAC CATGAAAATT
 GCCAAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATSTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCTGCA CACTGTGTCA
 ATCTTATCTG CTTTGCGTGC TCGTCAATT GGCC

EF077-4 (SEQ ID NO:296)

QPNWA YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSVE EINVGDENVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGEDELMSGSVNGDGS LKMAEKTVD SQYQTIIVNLV KESAAAPAHF VRLADRYAVP

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

FTLVAYLIAG VAWFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMGRES RHGVVVIKSGT
 MVEKLASAKT IAFDKTGTIT QGQLSVDQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
 VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTQESQETE KIDKTTIHIS
 RNGTHLGRIT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
 CLPQDKLTIL KELPKENHPV IMVGDGVNDA PSLAAADVGI AMBAHGATAA SETADVILK
 DDLSKVSQAV EIAQDTMKIA KQSVLIGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
 LSLARRRIG

EF079-1 (SEQ ID NO:297)

TAATTTCTAG CATCACCGAA GAAATTTTGA GAAAAACAAA GAGCCTGGGC CAATCACTGT
 CCCAGGCTCT CATGCTTTAT TTTTAAGGAG GAAGCAATGA AGTCAAAAAA GAAACGTCGT
 ATCATTGATG GTTTTATGAT TCTTTTACTG ATTATTGGAA TAGGTGCATT TGCCTATCCT
 TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
 AAAGCAAGCC AAGAAAACAC CAAAGAAATG GCTGAACTTC AAGAAAAAAT GGAAAAGAAA
 AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTTC TGAAACGCAA
 AAAACAACGA AAAAACCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
 ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
 AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTAGGAA TACACATGCG
 GTCATTTTCAG GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACABATTT GCCAGAAITTA
 AAAAAAGGCG ATGAATTTTA TATCGAAGTC AATGGGAAGA CGCTTCTTTA TCAAGTAGAT
 CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTAC ACATTGAGTC TGGCCAAGAT
 CTCGTCACTT TATTAAGTTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTTGA
 GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
 CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
 TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAAGTA G

EF079-2 (SEQ ID NO:298)

MKSKKKRRI IDGFMJLLLI IGIGAFAYPF
 VSDALNNYLD QQIIAHYQAK ASQENTKEMA ELQEKMEKKN QELAKFBSNP GLDPFSETQK
 TTKKPKDSYF ESHTIGVLT I PKINVRPIF DKTNALLLEK GSSLLESTSY PTGGTNTHAV
 ISGHRGLPQA KLFTDLPELK KGDEFYIEVN GKTLAYQVDQ IKTVETDTEK DLHIESGQDL
 VTLLTCTPYM INSHRLVVRG HRIPIYQPEKA AAGMKKVAQQ QNLLIMTLLL IACALIISGF
 IWIYKRRKKT TRPKP

EF079-3 (SEQ ID NO:299)

TCCT
 TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
 AAAGCAAGCC AAGAAAACAC CAAAGAAATG GCTGAACTTC AAGAAAAAAT GGAAAAGAAA
 AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTTC TGAAACGCAA
 AAAACAACGA AAAAACCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
 ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
 AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTAGGAA TACACATGCG
 GTCATTTTCAG GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACABATTT GCCAGAAITTA
 AAAAAAGGCG ATGAATTTTA TATCGAAGTC AATGGGAAGA CGCTTCTTTA TCAAGTAGAT
 CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTAC ACATTGAGTC TGGCCAAGAT
 CTCGTCACTT TATTAAGTTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTTGA
 GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
 CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
 TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAA

EF079-4 (SEQ ID NO:300)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. histolytica* Genes.

PF

VSDALNRYLD QQIIAHYQAK ASQENTHEMA ELQEKMEKKN QALAHNGSNP GLDPFSETQK
 TTKKPKDKSYF ESHTIGVLT I PKINURLPIF DKTNALLLEK GSLLLESTSY PTGGTNTHAV
 ISSHRLPQA KLFTDLPELF KSEDFYIFUN GKTLAYQVDE IFTWENTDTH DLHIESGQDL
 VTLLTCTPYM INSHRLLVRG HRIPYQPEFA AAGMKKVAQR TNLNLTLL IACALIISGF
 LIWYKREKKT TRKF

EF080-1 (SEQ ID NO:301)

TAGTTAACT GGTTTAGGCG TAGCAACGTT AGGCAATTTTC GTTGGACTCT TAGCACTCTT
 TTTATTAGGA GGTATTTCG TATGAAAAA GCAATTTTAC GTTATTTTTT CCTAATACTT
 CTTACCTTG GCGTTGCCCT ACCGCTTTCG GCGGCTGAAA ATGCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGCTTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGGCAAGG ACAAATATGC GATTCTTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGAAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GAGATAATAT GAGTCAAGGA
 AATTATTTCT GCGCTGCTCA AACCTTTGTT CAGGAAACTC AAGCATTGCT TAATAAAGGG
 GTTCCTGGGG GGCACATCG TGTGGACAGC GAAACAGGTA AATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAAACAA CTTTAAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTCATCACT
 ACGCGTCGTA TTCTTAAAA CAATGGCGCG AGTGGCGGAA TGGCGGCTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGCGCGGTC GAATTTTTTA G

EF080-2 (SEQ ID NO:302)

MKKR LLPIFFLILL TFGALPVSA AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFI VTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL
 IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFMAAQTFVQ ETQAFVNKGV
 PGGHYRVDSE TKGITRYKVI TPLEMVIAFA AALILSLVFL SINISKYQLK FSSYQYPFRE
 KTTLNLTSTRT DQLTNSFITR RRIKNNNGS GGMGGGGSTT HSTGGCTFGG GGRSF

EF080-3 (SEQ ID NO:303)

GGCTGAAA ATTCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGTCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGGCAAGG ACAAATATGC GATTCTTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGAAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GAGATAATAT GAGTCAAGGA
 AATTATTTCT GCGCTGCTCA AACCTTTGTT CAGGAAACTC AAGCATTGCT TAATAAAGGG
 GTTCCTGGGG GGCACATCG TGTGGACAGC GAAACAGGTA AATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAAACAA CTTTAAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTCATCACT
 ACGCGTCGTA TTCTTAAAA CAATGGCGCG AGTGGCGGAA TGGCGGCTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGCGCGGTC GAAT

EF080-4 (SEQ ID NO:304)

AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFI VTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFAAACTFVQ ETQAFVNKGV
 PGGHYRVDSE TGTKTRYKVI TPLEMVIAFA AALILSLVFL GINISFYCLK ESSYQYPFRE
 KTTNLNLSRT DQLTNSFITT RRIPKNNGGS GGMGGGGSTT HSTGGCTFGS GERS

EF081-1 (SEQ ID NO:305)

TGAATGGAAC GAAGCAATCG TAATAAAAAA TCTTCAAAAA AACCACTTAT TETTGGTGTT
 TCTGCCCTGG TTCTAATCGC TGCTGCCGGT GGCGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTAAAG CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAAG ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAAG ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAATC GCTTGGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTCGATTCAA GTAGATAATG CCAAACTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGGAAGCAN TCGCAATTA A

EF081-2 (SEQ ID NO:306)

MERSNRNKKS SKKPLILGVS ALVLIAAAGG GYYAYSQWQA KQELAEAKKT ATTFLNVLSK
 QEFDKLPSVQ QEASLKKNY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNEKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTESRYYPGL EAXRN

EF081-3 (SEQ ID NO:307)

T GGCGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTAAAG CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAAG ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAAG ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAATC GCTTGGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTCGATTCAA GTAGATAATG CCAAACTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGG

EF081-4 (SEQ ID NO:308)

G GYYAYSQWQA KQELAEAKKT ATTFLNVLSK
 QEFDKLPSVQ QEASLKKNY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNEKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTESRYYPGL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF082-1 (SEQ ID NO:309)

TAAAAAATGA AAAAGATGCT GCGCATTTCA AGCATTTTGT TGATCTCTAC GCGCTCTATG
 CTTTAAATA GTTCAAAAGT TGAAGCAGCT CAAGTGGCTT CATTGGAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ATCCACGAA CCCTTCTCAG
 CCGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGCTA CAGCTGACG CCGTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCTGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGGATTT TAAATAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTTGGCTGGA AATTATCACT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CCGCATTAAC GGTCCCAGTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CCGTGGCGGA CTGCGCTCTT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGAGCGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCTCG CGACAACGAA AAAAGTTGCA CTTAAACAAT ATAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT TTAA

EF082-2 (SEQ ID NO:310)

MKKIVRISS ILFVATPLML LNSSKVEAAQ VASIQSNADI TFALDNTVTP PVPNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNIHFGSK QIQAGTAIYS AILDVQNST GDILISVPNYV
 QVTDKRLNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATINSTQLL SLAPLTVPVT
 LDPTGAATSP VATAALSTGM GTWTLAFGSG XTAAQGIQLT VVATTKKVAA KQYKTTTLWI
 LDDTPL

EF082-3 (SEQ ID NO:311)

AGCT CAAGTCGCTT CTATTCAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ATCCACGAA CCCTTCTCAG
 CCGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGCTA CAGCTGACG CCGTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCTGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGGATTT TAAATAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTTGGCTGGA AATTATCACT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CCGCATTAAC GGTCCCAGTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CCGTGGCGGA CTGCGCTCTT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGAGCGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCTCG CGACAACGAA AAAAGTTGCA CTTAAACAAT ATAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT

EF082-4 (SEQ ID NO:312)

AQ VASIQSNADI TFALDNTVTP PVPNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNIHFGSK QIQAGTAIYS AILDVQNST GDILISVPNYV
 QVTDKRLNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATINSTQLL SLAPLTVPVT
 LDPTGAATSP VATAALSTGM GTWTLAFGSG XTAAQGIQLT VVATTKKVAA KQYKTTTLWI
 LDDTP

EF083-1 (SEQ ID NO:313)

TAATTTAAAA GACAAGGAGA AATAAAAATG AAAAAAGAAA TTTTAGCAGG AGCGCTTGTC
 GCTCTGTTTT TTATGCCTAC AGCTATGTTT GCGGCAAAAG GAGACCAAGG TGTGGATTGG
 GCGATTTATC AAGGTGAACA AGGTGCGCTTT GGCTATGCAC ATGATAAATT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT AACATATATA AACGCAAGTG
 GCAAGTGCTA TTGCCCAAGG TAAACGTGCG CATACCTATA TTTGCTATGA CACTTGGGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTCG CACCTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGACACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACTCTTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCTC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGCTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTGTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGCGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGGAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTGTAAA GTCAATGGAT CGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AATTATTAA

EF083-2 (SEQ ID NO:314)

MK KKILAGALVA LFFMPTAMFA AKGDQGVDA IYQGEQGRFG YAEKFAIAQ
 IGGYNASGIY EQYTYKTQVA SAIAQKRAH TYIWDYDWN MDIATTTMDY FLPRITPKN
 SIVALDFEHG ALASVPDGYG GYVSSDAEKA ANTEITLYGM RFTTLAGYTP MYYSYKPTFL
 NHVNYQQIHK EFPNSLWIAA YPIDGVSPYP LYAYFPSMDG IGTWTTTSAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEEIEK IPNSDVKVG D TVWVFNVDA WATGEAIPQW
 VKGNSYKQVE VTGSRVLEGG ILSWISKDGI ELLPDATVVP DHTDTHV V QYGETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NGSATSNVYT VRKSNLSSI AAKLGTTYQA
 LAALNGLANP NLIYPGQTLN Y

EF083-3 (SEQ ID NO:315)

AAAAG CAGACCAAGG TGTGGATTGG
 GCGATTATATC AAGGTGAACA AGGTGCTTTT GGCTATGCAC ATGATAAATT CGCTATTGGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT ACAGATATAA AACGCAAGTG
 GCAAGTGCTA TTGCCCAAGG TAAACGTGCG CATACCTATA TTTGCTATGA CACTTGGGGA
 AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTCG CACCTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGACACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACTCTTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCTC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGCTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTGTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGCGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGGAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTGTAAA GTCAATGGAT CGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* genes.

EF063-4 (SEQ ID NO:316)

KGDQGVDAW LYQGFQGRFB YAHDKFAIAQ
 LGGYNASGIY EQYTYKTQVA SAIAQGHRAH TYIWTDTAGN MDIAKTHMTY FLPRIQTPKN
 SIVALEFENG ALASVFDGYG GYVSSDAEKA ANTETILYGM BKIKQA WCH MYYSYKPFIL
 NHVNYQQIHK EPPNSLWIAA YPIDGVSPYP LYAYFPRMGG IGIMQW LAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEBIEK IPNSIVKNSD TUKVKFINDA WATGEAIPQW
 VKGNSYKVE VTGSRVLEQ ILWSISKDI ELLPDIATVP DKQFENHFW QYGETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NGSATSNVYT VKYGDNLSSI AAKLGTITYQA
 LAALNGLANP NLIYPGQTLN

EF084-1 (SEQ ID NO:317)

TAGTCAAACG TTTATTTTTC COTTAATCC AGAAAAAATC CCGTAAATTAT GSTACACTAC
 CTATTGAATT GGAGGAGAAC TATGAAGAAA TTTGATGTAA TTATTCTCGG TGCTGGGACG
 AGCGGTATGA TGGCCACGAT TGGCGCCGCC GAAGGAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGCTG GCGGCTGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTC AATTATCTG GGAATGAAAA ATTTTATATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTTA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTACGAA TTAGBAGTCA CTGTTTATTAC AAAAACACAG
 GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTGGCG TTGAAGCGCA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACCT AGCGGCGATA CCATGAGCCG GTCTCTACCCT
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGGCATA CCATGAGCCG GTCTCTACCCT
 ACCGAATCAC CTATTATTTT TGAAGAACCT TTTATCTGCG ATAAGAGCTT GAAAGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTTG AACCAGAAAG GAAAGCTTTT AATTATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGCC ATTTGAGGAC CTGCTGCTCT CCGCTGTTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAAATCAAC CTGTACCTCT AGCCTTGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCGTCAAAAC AACTAACAGA AAAGCAACGN
 CTTTCCTTTG TGGAACTACT GAAAGACTTT CAGTTTATTC TTACBAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CGGTGGGATT TCCCTCAAAG AAGTACCTCC TAAAACAATG
 GAGAGCAAAAT TAGTCAATGG TTTATTTTTT GCTGCTGAAC TTTTATATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTT GTCAGTGCAC ATGTTCTGCG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TCTAA

EF084-2 (SEQ ID NO:318)

MKKF DVIIVGAGTS GMMATIAAAE AGAQVLLIEK
 NRRVGKLLM TGGGRCNVTN NRPAEEIISF IPGNGFFLYS AFSQFBNYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNRIHEL GVTVFTKTQV TKLLHHEIQI IGVETELEKI
 YAPCVVLTG GRTPSTGAT GDGYKLAKKM GHTISPLYPT ESPIISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SBPAALRCSS FINQELTENG NQPVTVLADV
 FPTKSFEEVP AKQLTEKQRL SFVELLKDFQ FTVTHTLPLE KSFVTGGGIS LKEVTPKTIME
 SKLVNGLFFA GELLDINGYT GGYNVTAAPV TSHVABSHAA EIAHNTYLP I BEV

EF084-3 (SEQ ID NO:319)

C GAAGCAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGCTG GCGGCTGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTC AATTATCTG GGAATGAAAA ATTTTATATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTTA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTACGAA TTAGBAGTCA CTGTTTATTAC AAAAACACAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTEGCG TTGAAAACGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACCT GCGGCGCGCA CTTATCTTTC CACAGGAGCA
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGCGATA CCATCAGCCC GCTCTACCCCT
 ACCGAATCAC CTATTATTTC TGAAGAACCT TTTATCTTGG ATAAAACGTT GCAAGGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTTG AACCAAAAAG GAAAACCTTT AGTTAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGGC ATTTCAAGAC CTGCGCGGCT CCGCTGTTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAAATCAA CTGTCAGGCT AGCCTTGGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCTGCGAAA AACTAATAGA AAAGCAACGN
 CTTTCCTTTG TGGAACACT GAAAGACTTT CAGTCACTC TTATGAAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CGGTGGGATT TCCCTCAAG AAGTCAACCC TAAACAATG
 GAGAGCAAAT TAGTCAATGG TTTATTTTTT GCTGCTGAAC TTTTACATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTG GTCAGTGGAC ATGTTCTTGG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TC

EF084-4 (SEQ ID NO:320)

E AGAQVLLIEK

NRRVGKKLLM TGGGRCNVN NRPAEEIISF IPGNGKFLYS AFSQFINYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNIRINEL GVIVFTKTQV TKLEKNDQI IGVETELEKI
 YAPCVVLTG GRTYPSTGAT GDGYKLAKKM GHTISPLYPT ESPTISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SGFAALRCES FIMHLTENG NQPVTVALDV
 FPTKSFEFVP AKQLTEKQRL SFVELLKDFQ FTVTFTLPLE KSFVGGGIS LKEVTPKTME
 SKLVNGLFFA GELLDINGYT GGYNVTAAFV TGHVAGSHAA EIAVNTYLP IEEV

EF085-1 (SEQ ID NO:321)

TAACCCATGA AATCATTTTG TCCCGCATAT GGGGATATCA CTTTACCGGT GATGGCAGCA
 CAGTCCACAC TCATATCAAA AATCTGCGGG CGAAGTGCCG GAAAATATCA TCAAAACCAT
 CCGCGGTGTA GGTTACCGAT TGGAGGAATC ATTATAATCG AAGGAAAAGG GATTTTCATT
 AAGGTTTTTT CCTATACGAT CATTGTCCTG TTACTGCTTG TCGGTCTAAC GGCAACACTG
 TTTGCACAGC AATTTGTGTC TTATTTTCAGA GCGATGGAAG CAAGGCAAAC AGTAAAATCC
 TATCAGCCAT TGGTGGAACT GATTGAGAAT AGCGATAGGC TTGATATGCA AGAGGTGGCA
 GGGCTGTTTC ACTACAATAA CCAATCCTTT GAGTTTTATA TTAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCCGATACA TCAAATAGTG TTAGTCCCGA CTTTCTTTAT
 GTGGTACATA GAGATGATAA TATTTCGATT GTTGTCTAAA GGAAGGCGAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TCGGGGAATT GTTATGATTG CCAATATGGT TGTATTGAGC
 CTTTTATGCG CGTATATCTT TGCGCGGCAA ATGACAACGC CGATCAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAAA CCTGAAAGAA GTACCGCCGC CGTCTGAGCG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATCA GCTGAAAAGA AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTTGGAGG AAACACAGCG ATATTTCTTT
 GCGGCAGCCT CTCATGAGTT AAAAACGCCC ATCGCGGCTG TAAGGCTTCT GTTGGAGGGA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAGT ATCTGCGCA ATGCATCAAA
 ATGATGGACA GGCAGGGCAA AACCATTTCG GAAATACTGG AGCTTCTCAG CCTGAACGAT
 GGGAGAATCG TACCCATAGC CGAACCGCTG GACATAGGCG GATCTCTTGC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGCGGT TGTTCACAGA TATTCCAGCC
 GGACAAATTG TCCTGTCCGA TCCGAAGCTG ATCCAAAAGG CGATATCCAA TGTATATTG
 AATGCGGTTT AGAACACGCC CCAGGAGGT GAGGTACGGA TGTGAGTGA GCCTGGGGCT
 GAAAAATACC GTCTTTCCGT TTTGAACATG GCGGTTTACA TTATGATAC TGCACTTTCA
 AAGCTGTTCA TCCCATTCTA TCGCATTGAT CAGGCGCGAA GCGGCAAAA GTGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAAC GCTGGATGCC ATGAGCCTCC AATATGCGCT
 GGAAAAACACC TCAGATGGCG TTTTGTCTG GCTGGATTGA CCGCCACAT CAACACTATA
 AATATTTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF085-2 (SEQ ID NO:322)

MERKGIPIK
 VFSYTIIVLL LLNGVTATLF AQCFVSFYFA MEAQTTVESI QPLVELIQNS DRIDMQEVAG
 LFHYNNQSF E FYIEDKEGSV LYATPNADTS NSVRIDFLYV VHFDDNISIV AQSKAGVGLL
 YQGLTIRGIV MIAIMVVPSL LCAYIFARQM TTPIKALADS ANHMANLFEV PPPLERKDEL
 GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQFYFFA AASHLENTPI AAVSVLLEGM
 LENIGDYKDH SKYLRECIKM MDRQKGTISE ILELVSLNDS RIVFIAEPLD IGRTVAELLP
 DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPTQGGE VRIWSEPGAE
 KYRLSVLNMG VHIDTALSK LFIPFYRIDQ ARSSKKWAKE FGACHETENA GCHEPPICAG
 KHLRWRFVLA GFTAHINTIN I

EF085-3 (SEQ ID NO:323)

GC AATTTGTGTC TTATTTCAGA GGSATGGAAG CACAGCAAAC ACTAAATCC
 TATCAGCCAT TGGTGGAACT GATTCAGAAT AGCGATAGGC TTGATATGCA AGAGSTGGCA
 GGGCTGTTTC ACTACAATAA CCAATCCTTT GATTTTATA TTGAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCGATACA TCAAATATG TTAGGCGGA CTCTCTTTAT
 GTGGTACATA GAGATGATAA TATTTGATT GTTGCTCAA GCAAGGAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TGGGGAAAT GTTATGATG GATATAATG TGTATTCAGC
 CTTTATGCG CGTATATCTT TGCGCGGAA ATGACAAAGC GATCAAAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAA CCTGAAAGAA GTACCGCGGC GGTGAGAGG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATGA CCTCAAAAG AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTGGAGG AAACACAGG ATATTTCTTT
 GCGGACGCT CTCATGAGTT AAAAAGCGCC ATCGCGGCTG TAAGCTTCT GTTGGAGGGA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAT ATCTGGCGG ATGCATCAAA
 ATGATGGACA GGCAGGGCAA AACCATTTC GAAATACTG AGCTTCTGAG CCGAAGCAT
 GGGAGAATCG TACCCATAGC CGAACCGCTG GACATAGGBC GCAGGCTTC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGGCGT TGGTCACAGA TATTCAGCC
 GGACAAATTG TCCTGTCCSA TCCGAAGCTG ATCCAAAAG GGTATCTAA TGTATATTG
 AATGCGGTTG AGAACACGCC CCAGGGAGGT GAGGTAGGA TATGGAGTGA GGTGGGGCT
 GAAAAATACC GTCTTTCCGT TTTGAACATG GCGGTTACA TTGATATAC TGCATTTC
 AAGCTGTTCA TCCATTCTA TCGCATTGAT CAGGCGTGA GCAGCAAAA GTGGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAC GCTGGATGCG ATGAGGCTCC AATATGCGCT
 GGAAAAACAC TCAGATGGCG TTTTGTCTG GCTGGATTA CCGTCAAT CAACACTATA
 AATATTT

EF085-4 (SEQ ID NO:324)

QFVSFYFA MEAQTTVKS QPLVELIQNS DRIDMQEVAG
 LFHYNNQSF E FYIEDKEGSV LYATPNADTS NSVRIDFLYV VHFDDNISIV AQSKAGVGLL
 YQGLTIRGIV MIAIMVVPSL LCAYIFARQM TTPIKALADS ANHMANLFEV PPPLERKDEL
 GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQFYFFA AASHLENTPI AAVSVLLEGM
 LENIGDYKDH SKYLRECIKM MDRQKGTISE ILELVSLNDS RIVFIAEPLD IGRTVAELLP
 DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPTQGGE VRIWSEPGAE
 KYRLSVLNMG VHIDTALSK LFIPFYRIDQ ARSSKKWAKE FGACHETENA GCHEPPICAG
 KHLRWRFVLA GFTAHINTIN I

EF086-1 (SEQ ID NO:325)

TAAGTGGTGG GATTGGCAA TGGTTCGCG GCAGCGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTACTGC TCGCTGATG
 CTGTATGCAA AAGATCCAAA CATAAATGG CCAATTTATC GTGCAACAGG AGCTAACTTA
 ACAGATATTT CAATCACCCT TTAGGTACT GGAATTTTGT TAGAGATAA TCAACGCTTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTACAAGTAC AAGAAGCTGT TCCGTCGGTT TTAAAAAGTG TTTGCTTTGG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACACCGSCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTCCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTATTTTAAT GTTGTGGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAATA TTCCAGAGG GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGGT AAAAAGAACAA TACCTAATTI AACCTTAATT
 GCAAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTTCTTT AAAAAGACAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGGCTCA CTTGCGCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTTA CAGAAAAATA ACATATATSC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TATAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAAGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAAATG GTGCTTATAC AGGGAAACGC ACTGCGCAGT CATGCGTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAATAAATA GTATGGAAGG AATGAACTTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAAAATCA TTAATTTGCG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCTGCGATA ATGCGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GATTAATTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TCAATATGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATBAAGAAA TGGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CATTGGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATGCGAG GATCTATGCT GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTITATC GCTTAACTCT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GATTTCTTGA AGTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATATGCT GGGGTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAAACA ACTCTCAAG TAACTAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ATACGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGCGAG ATCAAAACAA AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CTTTGGGCA TGAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAAAGAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTCAACATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAA TACACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAATAA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCTAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAETTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF086-2 (SEQ ID NO:326)

LVGLANWFRA ALTDLILLH DDLNNTDAEK INFTAPLML YAEPIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEAQSVL KSVSSGDGLY FEGSLQHG YPYNGSYGNE
 LLKGFGRIQT ILQGSDEM N DPNISNLFNV VDFGYLQNLV NGHUPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFAPENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ FINEYAVGIS MEGQRVGN Y FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDREL ANQAYTGKRS PQSWVGSSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDAFIETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVCI EERSGEGYDI NEYFVNDKTY
 TNTFAKISK N YGKTVENGT YLTVVGKTN EEIALSLN K GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYFLTLANPL QNNASVSI EF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTHEALEK LIQEQEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TREVDFTNLL KIIKENEKHQ

WO 98/50554

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. coli* Genes.

EKDYTASSWE VYSEALKQAI THADTTTATT AEUHIAEHL EEFHILITLH NSGENKKEQK
 NGGNNGHLNT STGVDTGTGK QYKPSQGGF KPAK,ELPST SEPPIALVI IGLLVIASGC
 LLVFRKSKSK E

EF086-3 (SEQ ID NO:327)

ACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTCCTT
 CAACAAAGTG GGTCACTACTA TCATTTCTTT AAAAACCRA GAGTCTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCGTCCCAAG CGAATCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTA CAGAAAAATA ACGAATATGC GTGGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGAAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACAGGAA CGAATTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGG ACTGCTACT CAATGCTAGG TGGCTCAAAT
 AAT

EF086-4 (SEQ ID NO:328)

PENLRND IYTSIQTWLQ QSGSYHHFFK KPRDFEALIT
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KINNEYANGLS MYADYNGNVE FGNTENKKGW
 HTADJMLYLY NQDFAQFDES YWATIDPYRL PGTNDTREEL ANHAYTGKRS PQSWVGGSNN

EF087-1 (SEQ ID NO:329)

TAAGTGGTGG GATTGGCAAA TTGGTTCCGG GCAGGCTTAA GATATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AATTTAATTA AATTTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG GCAATTTATC GGTCAACAGG AGCTAACTTA
 ACAGATATTT CAATCACCGT TTTAGGTACT GCAATTTTGT TAGAAGATAA TCAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTAAGAAATG TTTCTCTGG TGATGGCTTA
 TATCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT AGAAGGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGTTTCCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTGTGATA AAGTTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGTTTCT GGTAGAAATA TTTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCACTACTA TCATTTCTTT AAAAACCRA GAGATTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCGTCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTA CAGAAAAATA ACGAATATGC GTGGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGG AGTCCCAAGT CATGCTTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAGATAAAA GATATGAAG AATGAACCTTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCTCTGATA AAGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATCTT GATTAGTTT AAGCGCAGCG
 ANTCATTGA ATAACATTGG CTATGTTTTT CCTAATTGNA TCAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTGG CTACGGAGAT ATTAACGAAT AATTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGCA AACTGTGTA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TGGGAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG GATTTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAATTTGCGA GACTGTATGC GTATGATCCA
 ATGTCCGTTA TTTGAGAAAA AATTGATAAC GGTSTTTATC GATTAATCTT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTGATAAGG GATTTCTTGA AGTAGTCGCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATAGTCC GGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAAACA ACTCCTGAAT TAACGAAGCA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACAGGCAAG CAGGTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAGCAAT AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCACCTTG TTGAATAAT TCAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAA TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGGAAAAAT AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAA CTAGCAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGCTC TTCTATTAAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF087-2 (SEQ ID NO:330)

LVGLANWFRA ALTDTLILLH DDLNLTDAEK LNKFTAPLML YAKFINIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEAIVPSVL KSVESGDSLY PQGSLIQHGY FPYNGSYGNE
 LLLKGFRIQT ILQGSWEMN DPNISNLFNV VDKSYLQLIV NGFMPSHVBO RSISRAPETN
 PFTTEFESGK ETIANLTIA KFAPENLRND IYTSIQTWLQ PQGSLYHFEK KPRDFEALID
 LKNVNVNSASP AQATPMQSLN VYGSMDRVLO KINNEYAVGIS MYSQRVGNH FGNTEKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDTEEL ANGAYTGKRS PQSWVGGSSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTDASIEETI LENRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLEVDI EERSGRYGLI NEYFVNDKTY
 TNTFAKISKV YGKTVENGTY EYLTUVGKTN EEIAALSHNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIET DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIIVKTT PEVTKEALEK LIQEPKENDQ KEYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TWENDTILH KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL ESNVFELEK NSGENKKEQK
 NNGNNHGLNT STGVDQGTGK QVKPSSQGGF RKASQFLPST GEKFSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF087-3 (SEQ ID NO:331)

A ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGCTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTGNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTGC CTACGGAGAT ATTAACGAAT ACCTTCTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTCTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TGCAGCTTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG GCATTGAGGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAATCTT TGCGAATCCT
 TTACAAAATA ATGCATCC

EF087-4 (SEQ ID NO:332)

NRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLEVDI EERSGRYBDI NEYFVNDKTY
 TNTFAKISKV YGKTVENGTY EYLTUVGKTN EEIAALSHNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNAS

EF088-1 (SEQ ID NO:333)

TABLE 1. Nucleotide and Amino Acid Sequences of *A. taeniorhynchus* Genes.

TAACTGGTGG GATTGGCAAA TTGGTTCCGC GCAGAGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AATTTAATAA AATTTACAGC TCGGTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTAAT STGCACAGG AGTTAACTTA
 ACAGATATTT CAATCACCGT TTTAGGTACT GGACCTTTCT TAGAATATAA TTAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCGGTT TTAATAAGTG TTTCTCTTCA TGAATGCCTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTGGTT ATAACTGCTA TTAACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTGAG ACTATTTTAC AAGSTTGGGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GGTSTGATA AAGSTTACCT ACAAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTABAATA TTTCCAGAGC GGCAGAAACG
 AATCCTTTTA CTACAGACTT TGAATCCGGT AAAGAAACAA TAGCTAATTT AADTTTAATT
 GCAAAATTTG CACCAGAAAA TTTAAGAAAT CACATTTATA CATCTATGCA AATSTGGCTT
 CAACAAAGTG GGTCACTATA TCATTTCTTT AAAAAACCA GAGACTTTGA AGCTTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA TCTGCTAAG CAGACAGAA GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCTTA CAGAAAAAT ACCAATATCC GGTGGGATC
 AGTATGTATT CACAACGTGT CCGAAACTAT CAATTTGGTA ATACGAAAA TAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CAGACATTTA CAAAGAGAAA
 TTGGCAAAATG GTGCTTATAC AGGGAAACGC ACTCCCACT CATGGGAGG TGGCTCAAAAT
 AATGGACAGG TTGCCTCTAT AGGAAATGTT TTAGATAAAA STAATCAAG AATGAACCTA
 GTTGCTAAAA AATCTTGCTT CTTATTAGAT GGTCAAAATA TTAATTTGAG AATSTGGCAT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ACCGATCAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATCTCT GCAATATTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TGAATACGCT TSATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTGCTAA AATTAGTAAA AATTATGGCA AACTTTTGA AATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAA CCAATTGAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCA GACTGTATGC GTATGATCCA
 ATGTCGCTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GGTAACTCT TGGGAATCCT
 TTACAAAAATA ATGCATCCGT TTCTATTGAA TTTBATAAGG GCATTTCTGA ACTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATATGTC CGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTAAAAACA ACTCTGAGG TAAGGAGAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT AATCCGCAAG CAGCTGGAAG
 GTCTACAGCG AAGCAATGAA ACAAGCACAA ACTGTGBCAG ATCAAAACAC ACCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTGCGCAG TSAAGCAATT GCTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTSAAAATCA TCAAGAAAA CAGAAAAAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGTAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAAATBTG CCGAAAAATA AAAGGAGCAA
 AAAAAATGGG GGAATAATGG ACCTTAAAT ACTATATAG GATTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAAAAAAG CTAGCCATTT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGIG ATTATTGCTC TTTATATTAT CCGCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF088-2 (SEQ ID NO:334)

LVGLANWFRA ALTDTLILLH DDLNNTDAEK LNHFTAPLML YAKDPKQWP IYRATGANLT
 DISITVLGTG LLLLEDNQRLV QVQEAVPSVL KSVSSGGGLY PEGSLICHOY FPYNGSYGNE
 LLKGFGRQIT ILQGSWEMN DPNISNLFNV VDKGYLQLMV NGKMPSHNSG RSISRAPETN
 PFTTEFESGK ETIANLTIA KFAPENLND IYTSIQTLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KNNEYAVGIS MYSQRUCNVE FBNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTIVDTREL ANGAVTQRS PQSWVGGSNN
 GQVASIGMFL DKSNEGMLNV AKKSWFLLDG QIIMLGSGIT GTTDASLETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMTLEWQI EERSGNGDI NEYFVNDKTY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TNTFAKISK N YGKTVENGTY EYLTVVGKTN EEIAALSHNK GYTALENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVNIET PKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEQRHHEQ FDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TREVDKTNLL HIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAYKELTEK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKKSLALVI IGLLVIASGC
 LLVFRKSKSK K

EF088-3 (SEQ ID NO:335)

A ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGGAG ATCAACCAAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTGGGAG TBAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAGAAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA CTBAAGCAATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TABACCAAGC AGAAGCAAAA
 CTACGTTGCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GGAATAATTA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG AACTTTAAAT ACTAATAGG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCABAAAAG CTAGCCATT TTTACCGAGC
 ACAGGAGAAA AGAAA

EF088-4 (SEQ ID NO:336)

T PEVTKEALEK LIQEQRHHEQ KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVHVP TREVDKTNLL HIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAYKELTEK NSGENKKEQK
 NGGNNGHLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKK

EF089-1 (SEQ ID NO:337)

TGACAGATAC ACCTGCTAAC ACAGGAAACT AAGAACGACA GCATATACGC AAGATCGGGA
 TATAGGTCAA AAATTTTTTG GCTTATCTTT CGGTCTTTTG GTCTTTATAA TACAACAAAG
 AATGACAGAC ATAGGAGAAT GAATATGAAC AGATGGAAG TATATGCAAC GGTAATCGCT
 TGTATGTTAT TTGGCTGGAT TGGCGTGGAG GCGCAGGCTT CTBAATTTAA TTTTGCGGTC
 ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATGAAAAA CCTACTTTTA CTAAAAATG
 GCGCCTGGTG CCAAACAAAC CGTAGAAATT CAGTTACGCA ATGATACABA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGTCGTAGT AGAATATGGC
 CAAAACGGGA TCAACCTGA CAAACCTTA CGTTTAACT TAAAAGATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTC CAAAAGACCT TACCTTTAAC CATTACGATG
 CCTAAAGATT CTTTTGATGG CGTGATGGCT GCGGTATAA CACTGAAAGA GAAAAAGAAA
 GAAACAACGA CTTCTGCGGA TCAATCAAAA GGGTTAGCTA TTAATAATTA ATACTCCTAT
 GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTT AACCAATTTT AAAATTACTG
 GGGGTTAAAC CAGGCCAAGT CAACGCGCGA AACGTCATCA ATGTTTCTTT ACAAACCCA
 CAAGCGGCCT ATTTAAACCA ATTACATTTA ATCAACACTT TTCAAAAGG AGCGGAAACG
 CTTTACCAAT CCGATACTGA GGATATGCAA GTGGCGGCAA ACTCTAATTT TAGTTACCCA
 ATTTCTTTAA AAGGGGAACG ATTAACGCCA GGAAATATG TCTTGAAATC AACGGCCTAT
 GGTGTAAAAG ATGAAAAGGG CACCTATCAA GTCAAAGGCT CCAATGCTTA AGAACGGTAC
 CTGTACAAAT GGGAAATTAC AAAAGAATTT ACTATTTCTT GGGACGTCGC TAAAGAATTA
 AATGAAAAAG ACGTAACCAT TAAAGGAACC AATTGGTGGT TGTATCTACT GATTGCATTA
 ATCATTCTAG CGCTGCTCTT ATTGATTTTC TTCTTGTTAT GTAAAGAGAA AAAAGAGGAA
 GAACAACAAT CTGAGCAATA A

EF089-2 (SEQ ID NO:338)

TABLE 1. Nucleotide and Amino Acid Sequences of *A. taeniosomae* genes.

MEF WKVYATVIAC

MLPGWIGVEA HASEFNFAVT PTIPENQVDF SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT
 IENTVNSATT NLNGVVEYQG NGIKPDKTLR FNLKDTVEA KHLILVNSQ KTLPLTITMP
 KDSFDGVMAG GITLKEKKKE TTTSADQSKG LAIINNEYSVV VAILLIDNET KVQPDLLKLG
 VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGSETL VQSDTEHMQV APNSNFSYPI
 SLKGERLTPG KYVLKSTAYG VKDEKGTQV HANGHEBETL VWEFTWEPT ISSDVAKELN
 EKDVTIKGTN WWLYLLIALI ILALLLLIFF LYRKKKKREE QCSQ

EF089-3 (SEQ ID NO:339)

T CTGAATTTAA TTTTGCGGTC

ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATCAAAAA CTTACTTTGA CTTAAAAATG
 GCGCCTGGTG CCAAACAAAC COTAGAAATT CAGTTAGGTA ATGATAGGTA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTAA ATGCGCTACT AGAATATGGC
 CAAAACGGGA TCAAACCTGA CAAAACCTTA CTTTITAACT TAAAAATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTCC CAAAAGACT TACCTTTAAG CATTACGATG
 CCTAAAGATT CTTTATATG CGTGATGGCT GCGGTATTA CACTCAAGTA GAAAAAGAAA
 GAAACAACGA CTTCTGCGGA TCAATCAAAA GCTTAGCTA TTATTAATTA ATACTCCTAT
 GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTG AACCAGATT AAAATTACTG
 GGGGTTAAAC CAGGCCAAGT CAACGCGCGA AACGTGATCA ATGTTCTTTT ACAAACCCCA
 CAAGCGGCTT ATTTAAACCA ATTACATTTA ATCAAGACTT TTCAAGAGG AGCGGAACG
 CTTTACCAAT CCGATACTGA GGATATGCAA GTGGGSCCAA ACTTAACTT TAGTTACCCA
 ATTTCTTTAA AAGGGGAACG AT

EF089-4 (SEQ ID NO:340)

SEFNFAVT PTIPENQVDF SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT

IENTVNSATT NLNGVVEYQG NGIKPDKTLR FNLKDTVEA KHLILVNSQ KTLPLTITMP
 KDSFDGVMAG GITLKEKKKE TTTSADQSKG LAIINNEYSVV VAILLIDNET KVQPDLLKLG
 VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGSETL VQSDTEHMQV APNSNFSYPI
 SLKGER

EF090-1 (SEQ ID NO:341)

TAGTCTCTAA GAAATAAACC TAAAAATTAT GATATAAAGG ATGAGCAAT GAAAAAGAA
 GAAATGCAAA TGCCTAATAC ACGTCGTCAA AAATCAGGAA AAAATAATTA AAAGAAAGTA
 ATTATTACTT CTTTGGTTGG ACTAGCTCTG GTTGCTGGCG CCACTATGT TTATTTTCAA
 AGTCACTTTT TNCCAACCAC AAAAGTAAAT GGAGTTTCTG TAGGCTTCTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACCGAAG AAGTTCTGCT TCAAACGGGG
 ACAAAGAAG AAAAATTCA ACTTCCTAAA AAATACGAT TGTATCAAAA ATTTTAAAAA
 GACCATTTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAAG AGGCATTTAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTTCGA GAGGCGAAG CAGCAAAAA TGCGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATTCTT CCCGAGAAC AAGGCATAGT AGTGGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTGAAGCGG CAAAAGGCAA CTATCAATAT
 AATGCCAAG AGTTTTTATA AGCCCTGAA ATTACAAAG AGGATCAAC GTTAAAGCA
 ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CAGTTATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAAC ACAAATTCAA AACGTGCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACTACTTG GGTGACACAA TTAGAAACAA CATATGCTTC TGCTAATCAA
 CCAGTTTAT TTACAGATGT TCACGGCAGG ACACGTCTTT TAAAAACAA CGGAAGTTAT
 GGCTGGTGA TTGATGGGGC CAAAACGCAA GAACCTACTAG TAAACGCGCT AATAGCCAA
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGCTGATA CCAAGAAAA TAGTAAATTT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAA TGTATTTTTT CATTGATGGC
 AAAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGAAC CGCAACAGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGGATTCC ATACAATTTT ATATCGGACA ACGATCTTA ACTTAAAGC TCAAATGCTT
 GATGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATTC CTTATTAAAG TCAAGGGGGC
 GTTGTACAC AAATCGGGAT TCATGACTCC GACCATAAAT TCATTAAGTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GCTGTATCA ACAGCGTAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCTGCTAA TTATTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTAGC GCGAAGAAG ATAA

EF090-2 (SEQ ID NO:342)

MRNTRRQK SGKNNKKVI ITSIVGLALV AGGSYVYFQS
 HFXPTTKVNG VSVGWLVNVA AEEKLAQVNG TEEVVVQTGT FHEKIQLEKH YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSHNASIR FNGGTFEIVP EEQGTVVDTQ
 RLNQIIADV EAGKGNVQYN AKDFYKAPEI TKEEQTLKAT LTTLNKLNK TITVDINGEK
 VAFDKTQIQN VLNDDGTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGT FRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSRIA NNYIEIDLD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGGQILD GSEYSVPKY WMPLLSQGGV
 VTQIGIHDS HKLDKYGDKE AFKTDAGSNG CINTPSTENS KIFDVSIDGM PVIIYGHYD
 DAPGEFDKPV DYGEV

EF090-3 (SEQ ID NO:343)

CAC AAAAGTAAAT GGAGTTTCTG TAGGCTGGTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACGGAAG AAGTTCTGGT TCAAACGGGG
 ACAAAGAAG AAAAAATTCA ACTTCCTAAA AAATACCAAT TCGATCAAAA ATTTTAAAA
 GACCATTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAAG AAGCATTCAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTCCA GAGGGAAGC CAGGCALAAA TCGGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATTGTT CCGAAGAAC AAGGCAAGT AGTGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTCAAGTNG GAAAAGTCAA CTATCAATAT
 AATGCCAAAG ATTTTATATA AGCCCTGAA ATTACAAAAG AAGATCAAC GTTAAAGGCA
 ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CATTCTATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAC ACAAATTCAA AACCTCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACACTTG GGTGACACAA TTAGAAACAA CATATCTTTC TGCTAATCAA
 CCAGTTTTAT TTACAGATGT TCACGGCAG ACAGCTCTT TTAAAGACAA CGGAAGTTAT
 GGCTGGTCGA TTGATGGGGC CAAAACGCAA GAAGTATAG TAAAGCGCT GAATAGCCAA
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTCTCTATA CCAAAGAAA TAGTAAATTT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAA TGTATTCTTT CATTGATGGC
 AAAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGAAC CGCAACAGTA
 CCAGGATTCC ATACAATTTT ATATCGGACA ACCGATCTGA ATTAGAAAG TCAAATGCTT
 GATGGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATTC CTTATTAAAG TCAAGGGGGC
 GTTGTACAC AAATCGGGAT TCATGACTCC GACCATAAAT TCGATAASTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GCTGTATCA ATACGCGAG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCTGCTAA TTATTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTAGC GCGAAGAAGT AT

EF090-4 (SEQ ID NO:344)

TKVNG VSVGWLVNVA AEEKLAQVNG TEEVVVQTGT FHEKIQLEKH YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSHNASIR FNGGTFEIVP EEQGTVVDTQ
 RLNQIIADV EAGKGNVQYN AKDFYKAPEI TKEEQTLKAT LTTLNKLNK TITVDINGEK
 VAFDKTQIQN VLNDDGTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGT FRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSRIA NNYIEIDLD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGGQILD GSEYSVPKY WMPLLSQGGV
 VTQIGIHDS HKLDKYGDKE AFKTDAGSNG CINTPSTENS KIFDVSIDGM PVIIYGHYD

TABLE 1. Nucleotide and Amino Acid Sequences of *E. parvum* Genes.

DAPSEFDKPV DYGEEV

EF091-1 (SEQ ID NO:345)

TAATIGGNGG AGATTTTAT GGCTAAAAAA GGTGATTTAT TTTTAAAGG AGTAATTGGT
 GGAACAGCAG CAGCCGTGCG CGCATTATTA GTTGAATTA AATTAGTTAA AGAATTACGT
 GATGATTTAT CAAATCAAAC AGATGATTTA AAAACAAAG CGTACATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGAAAGC AAAAGGCGG CGTTTATCA
 GATCAAGCCT CTGATTGCGC AGGTTCTGTC AAAGAAAGAA CAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGTAT AATTGATTA AATAGAGAG TGATTTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATTAAG CAGAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GAGGTTAAG ATTCTGCGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA AATAGAAAT CCAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTAAAGAT GCAGCAAGC AGCTAAAAA AGAATTTAAA
 GGGTAA

EF091-2 (SEQ ID NO:346)

MAKKG GFPLGAVIGG TAAVAALLL APKSGHELEI ELNQTDELEI NKAQDYTDYA
 VQKGTETLEI AKQKAGVLSD QASDLAGSVK ETKUSLEKA QGUSGEMLDN FKKQTGDLSD
 QFKKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKKEFKG

EF091-3 (SEQ ID NO:347)

AT CAAATCAAAC AGATGATTTA AAAACAAAG CGCAAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGAAAGC AAAAGGCGG CGTTTATCA
 GATCAAGCCT CTGATTGCGC AGGTTCTGTC AAAGAAAGAA CAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGTAT AATTGATTA AATAGAGAG TGATTTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATTAAG CAGAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GAGGTTAAG ATTCTGCGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA AATAGAAAT CCAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTAAAGAT GCAGCAAGC AGCTAAAAA AGAATTTAAA
 GGGTAA

EF091-4 (SEQ ID NO:348)

SNQTDLLK NKAQDYTDYA
 VQKGTETLEI AKQKAGVLSD QASDLAGSVK ETKUSLEKA QGUSGEMLDN FKKQTGDLSD
 QFKKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKKEFKG

EF092-1 (SEQ ID NO:349)

TAAGGGGATG AAGAAAAAAT GGCAAAAAAA ACAATTAT AT TATTTTTC CGCAGGAATG
 AGCACGAGTT TATTAGTAAC AAAAATGCAA AAAGCAGTAG AATATGTTGG CATGGAAGCA
 GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAAAT TGATGATTA AGAGGTGAAT
 GTTTTACTTT TAGGTCCACA AGTTCGTTTC ATGAAAGGCG AATTGATTA AAAATTACAA
 CCAAAGGGA TTCCTTTAGA TGTAAATTAAC ATGGCAGATT ATGGCATGAT GAATGGCGAA
 AAAGTTTTAG ATCAAGCAAT CTCATTAATG GGATAA

EF092-2 (SEQ ID NO:350)

MAKKT IMLVCSAGMS TSLLVTKMQK AEDRGMEAD IFAVSASEAT TNLENKEVNV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LLLGPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMENGEK VLEQALSLMG

EF092-3 (SEQ ID NO:351)

AG AAGATCGTGG CATGGAAGCA
GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAAACT TGGAAAATAA AGAGGTGAAT
GTTTTACTTT TAGGTCCACA AGTTCTTTTC ATBAAAGGUC AATTGAAACA AAAATTACAA
CCAAAAGGGA TTCCTTTAGA TGTAAATTAAC ATBGEAGATT ATGGCATBAT GAATGGCGAA
AAAGTTTATG ATCAAGCAAT CTCATTAATG GGA

EF092-4 (SEQ ID NO:352)

EDRGMEAD IFAVSASEAD TNLENKEVNV
LLLGPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMENGEK VLEQALSLMG

EF093-1 (SEQ ID NO:353)

TAGTTTTTTT CCGATAAAGG GAGAATTTTA ATGAGGCAAA AATATTCAGG AAACCTTATTG
TTCACGGCCA TGGCCATTGT TTATTTGATG AGTTTCTG CCCTTCAGTT ACTAGAAGAA
CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGCAAT ACTATGCAAG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATGCAAAA ATGACCAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAS AGAGACTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGGA ATAG

EF093-2 (SEQ ID NO:354)

M RQKYSNLLF TAMAIVYLS FLALQLLEER QLTQKFTQAT QEYYAGKSIF
HLFLADVQKN RRKLKTEERL VYAQVTLDT YHNEQLRITV LLNKSGRKYQ YQERVSHQKK
AETILE

EF093-3 (SEQ ID NO:355)

CCTTCAGTT ACTAGAAGAA
CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGCAAT ACTATGCAAG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATGCAAAA ATGACCAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAS AGAGACTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGG

EF093-4 (SEQ ID NO:356)

LQLLEER QLTQKFTQAT QEYYAGKSIF
HLFLADVQKN RRKLKTEERL VYAQVTLDT YHNEQLRITV LLNKSGRKYQ YQERVSHQKK
AETI

EF094-1 (SEQ ID NO:357)

TAAACATTTG AGACATTCAG AGGTGAATGT CTCTTTTTTA TTAATCAAAA ACGAAAGGGG
ATTAATTATA TGAAAAAAC AACATTTAAA AATTGGTGGT TATTTGGGAC TTTGGCTCTA
TTAAGTCAAA CAATTGGCGG AACGATTGCT CCTAAGATG CTTTTGCGA TGAAATTACT
CACCCCTAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAGT TGACGGAACT
TTTAGCGATG GCAGCAGCT CTCAGAAGCT ACTAGTGTAT TATATGAGA ATACAATGCT
GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCCAAACGA AGTGACGCAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. coli* Genes.

```

GGTTATCAGA AAAACCCCTTT GCCATCAATG TCTATAAAG CAAATCAAT ATCCGTTCTT
TGGGAAAAAG CTGGAACAGA TATTGATAGG AATTATCTTG CAGAAAGGAT GATTGTGGGAA
GAAGTGAACG GTTATAAACT CCATTCGATA AAAAGATTAG STGCTCTTC AGTTGATATA
AAATCTATTG AAGGAAAAAT TAATAGGGCA ATTATAGGAT ATCAATGAAA ACCAAGTTTT
CATAATACCA CTGTAAAAAC AATTTTAGST CAATGAAA GAATTAATGA TAAAAATGAA
TTAAATTTAT TTGAGTTTGA TAAAGTGTG CAAATATGCB CCAATATAGA TTACCGTGTA
ATTGGGAATC AATGAGTGCT TACTTCAAAE TCTAATGGA AATCAAGAAC ATTAACATTG
AAAAAATCAG CTGCTACTTG AACTGCACTG CCTTATAGAA AAGCAAGACT TCAAACTGTG
ATGGCTGGTG CGCTTGATAA GCGCAATGCG TACGCTATTA AAATTAATGT GGAAGACTAG
GCTTCTTTAA AGATCAAAAA AATCGATGAA CAATGAGTG ATATTGTACC AGAAACGGTT
TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAATATAG TGATATAGA TAAAGATGGG
ATTTCTATTT TGGATGGAAT TCCGATGCTG ACAAATGTA CTATTACTGA AAAATCGGTG
CCAGATCCTT ATATGATTGA TACGATGCTG ATGCTGCTGA CCAATTAAGC GCGCGAGACC
ATTTCCATGA CTTCGAAAAA TATCGGAA AAAGCTGCTGA TGGCTTGA GAAGACTGGG
GTABAAACAG GTACTGATCT TTGGAAGGAG AATTATCTG TACTGAAAA TACATTGGCC
ATTCGTAAAG ACAGCCCACT TGCTGAATTT CTTCAAGAAA TACATGCGGA TAAAAAGGT
CGTSCGGAAA CACCAAAAGA GCTTCTAAT GCTTCAAGC TGGGAAGCTA TTACGTGACA
GAAACAATCT CTAGTAATGG TTTCTGGAAT AGCTTGAAG CAAGAAAGT CAGATTAAAA
TATGCAATC AAACCGTGGG TCTTCTTACC AGTAACTAA AAGGTAAGAA CAAAGAAATT
ACTGSGGAAA CCACTTTGAC AAAAAGAGAC AAAGATAGCG GTAAATGAG TAAAGGGAAA
GCTGAGTTTA AAGGAGCTGA ATATAGCTG TTTACTGCAA AAGATGCTCA AACTGTAAAA
TGGAGTGAAG CTTTTAAAC AGAATTAGTG AAGGGAAGCA AAGCTGCTGA TGAACAGTG
ACTTTGGCTT TAGATGAAAA GAACCAATTT GCGCTTGAAC AGCTAGCAAT TAACGACTAT
TTCTGGCAAG AAACCAAAAG ACCTGAAGGA TATAGCTTG ATGAAGGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACAAAAA AATGCTGAA TACTGGAZA TTTTACGGCA
AAAGAACAAG TTATTGCTT TGGCTTTGAT TTTTCTGAT TTTCTGATG GCTGATGGC
ACTGCCGAAA CTGGATTAA CGACTTATCT CTGAAAGCT GCGCTGCTGA AAGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGCGACC ACAGCTGATA ACGAGCAAT AGGTTTTCAT
GGCTATGGTA AGTTTGAAAA TCTTCTTAT GGGTATATTT TATTGAGAA AATAGAGGCT
CCAGAAGGAT TTCAAAAGAT TACAGCAATA GAAATGCTTT CTACATTTAA GAAAAACAA
GACGACTATG CGAAGAGTGA GTATGTCTTT ACCATTAAGS AAGAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAACTAACA ACAGATTTTC TGTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCTGAG AAAGAGATA GTTTGACTTC TTTTGGGACT
TGGAAAGACG GAAATAAAAA ATTGAATACC CTTBATTTCA CCGAGGTAGT TGATAAATTG
AGATATAACT TGCATGAAAT CAAAGAAGAC TGGTATGCTG TAGCTCAAGC CATTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAGAGCTA AATGCTGCTG GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAATTT GGAATTTCT GATATAATTA
ACCGCTGAAC AAGTTTTGGA TAAAAAGATC GTCTTCTTCA ATTATCTTA TGAACAACAG
GTAGCCTTTG AAGCAGGCAA TGAGCACTA GCGAGGCTAG CTAGCTGAA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACGCTAT GTTTCCTATC AAGCAAAAGC CCACCTAGAA
GATGGTTCGC AAACCTTTAC TCATGCTGAC TGTATGATA TTTTCTATGA TGTGTGCGTT
ACCCATGATG TACTGGATGG CTCAAAAGAA CTTTCTGAAA CAATTTTCTA TGCTTTACTA
CCAGATGGTA CGAACAAGAA AATTTGGAAT TCTGGCAAAA TTGAGCTTGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGGGAAA AAGTAGATA CCGGAAGATA TCCAGAAGGA
ACTAAGTTTA CTTTTACGGA AATCAATTAC GAAAAAGCTG GAAAGCTGAA TGAAGAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAGCC TTAAGAGTAA AAGAGCTGCC AACCATACCG
AGTACGCCAA AACAACCGGA AACACAGCT GTTCAAGTA ATTCTGAGA ATCTAGTCCC
ACAGTGAAGA CATTCGCCGA AACTGGGAG AAAAATTGCA ACCTTCTACT GTTAGTTGGC
TTTATCTTGA TTTTTCGAC TGCTGGGTAT TACTTCTTGA ATGCGGCAAA TTAA

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EF094-2 (SEQ ID NO:358)

MKKTTFKN WSLFATLALL SQTIGGTIGP TIAFADRIH

PQEVTHYDV SKLYEVDGTF SDGSTLSEPT TSLNATYGA KCTTHTEPG VSIPTVTHG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YQKNPLPSMS DKAKLVSVLW EKAGTI IDTN MVAQKMIWEE VNSYHLHSIK FLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKTLGQ STTLIDNHEL NLSEFNWVQ NTANIDYRVI
 GNQLVLTPTS NSKSGTLTLK KSAGTSTPVA YKPAQLTTH AGALENPNTY AIKINVETKG
 SLKIKKIDKE SGDIVPETVF HLDFGHALPS KLVTHDEHI SILENPHST FVTITEKSV
 DPYIMDTTPM AATIKAGETI SMTSPHMQK GQILLEKTSV ETSTELWNNH YSLAGNTFAI
 RKDSPAGEIV QEITTDKGR AETPHFLANA LELGTYVTE TKSSNGFVHT PKPTKVELKY
 ANQTVLVTN NVKQONQEIT GETTITKEDY DTQIESQCHA EPKGAETTLF TAKDQAVKW
 SEAFKTELVK GTKASDETVT LALDEFHQVA VHLAINETV WQETRAPEGY TLDETKYPVS
 IKFVDNNEKN AVITRDVTAK EQVIRFGDF PEPASSAGST AETGFNDLSF KVSPLGTXE
 ITGAEDKATT ACNEQLGFDG YGKFENLPAG DYLLSEIEAP EGDHITPLE IRSTFKENKD
 DYAKSEYVPT ITEEGQKQPI FMVTVFYEKI TINHEFVWLD RLIDNDELPEK EDSLTSLATW
 KDCNKKLNTL DFTELVDKLR YNLHEIKEDW YVVAQIEVE ATPAAQEKDE KAKPVVIAET
 TATLANKEKT GTWKILHKLK AEQVLDSHIV LIDNTEYEFV AFEAGNEPVA KDASLNNQAQ
 TVNCTIERHV SIQTKAHLED GSQTFTHGIV MDHFDNVCVT HDNLLSKKEA PETILYALLP
 DGTNKEIWKI GKIEHEVNDK EFTKIVLAKF VDTGNYFEST KFCNTEINYE HDGIVNGKHN
 EDLKEKSQTL TPKEVPTIPS TPKQPETPAN PCHNSPRAHT MKTDTCTSEK NSNVLLLVGF
 ILIFSTAGYY FWNRRN

EF094-3 (SEQ ID NO:359)

CGA TGAAATTACT

CACCCCTCAAG AGGTAACAAT TCATTATBAC BTAAATAAAC TGTATGAGCT TGACGGAACCT
 TTTAGCGATG GCAGCACGCT CTCAGAACTT ACTAGTTCAT TATATGCAGA ATACATGGT
 GCAAAACAAA CAGTATTTTG TATTGAACAA GGTGTTAGTA TTCTAACAGA AGTGACGCAC
 GGTTATCAGA AAAACCCCTTT GCCATCAATG TGTGATAAAG CGAAATAGT ATCGGTTCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGCTT GAAAAAGAT GATTTGGGAA
 GAAGTGAACG GTTATAAACT CCATTTCATA AAAATATTAG GTGTTCTTTC AGTTGATATA
 AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGATAGCT ATCTAAAAAA ACCAAGTTTT
 CATAATACCA CTGTAAAAAC AATTTTAGCT CAATTBACAA CTTTAAATAGA TAAAAATGAA
 TTAAATTTAT CTGAGTTTGA TAAAGTCTTC TAAAAAGCG CGAAATAGTA TTACCGTGTA
 ATTGGGAATC AATTAGTGCT TACTCCAAAC TTTAATTGCA AATTAGGAAC ATTAACATTG
 AAAAAATCAG CTGGTACTGG AACTCCAGTC GTTATATAAA AAGCAGGACT TCAAACGTG
 ATGGCTGGTG CGCTTGATAA GCCCAATAAC TACGTTATTA AAATTAATGT GGAAACTAAG
 GGTCTTTTAA AGATCAAAAA AATCGATAAA GAATCAGGTC ATATTGTACC AGAAACGGTT
 TTCCATTTAG ATTTTGGGAA AGCTTTAGCT TAAAAAGATG TGACAAACAGA TAAAGATGGG
 ATTTCTATTT TGGATGGAAT TCCCCATGCT ACAAAGGTAA CTATTACTGA AAAATCGGTG
 CCAGATCCTT ATATGATTGA TACCACACCC ATGGCTTCCA CCATTAAAGT GGGCGAGACC
 ATTTCCATGA CTTGCAAAAA TATGCGACAA AAABBTCAAA TTTTCTTAGA GAAGACTGGG
 GTAGAAACAG GTACTGATCT TTGGAATGAT AATTATTCTC TATCTGGAAA TACATTTGCC
 ATTCGTAAAG ACAGCCCAGC TGGTGAAATT TCCCAAGAAA TATCTAGCGA TGAAAAAGGT
 CGTGCGGAAA CACCAAAAAGA GCTTGCTAAT GTTTTGGAAC TGTATCTCTA TTACGTGACA
 GAAACTAAAT CTAGTAATGG TTTCTGTAAT ATTTTCAATC CAACTAAAGT CGAGTTAAAA
 TATGCCAATC AAACCGTGGC TCTTGTTATC AATAAGCTAA AATTTTAAAA CCAAGAAATT
 ACTGGGGAAA CCACCTTTGAC AAAAGAAGAT AAAGATCTCT CTATCTAGAG TCAAGGGAAA
 GCTGAGTTTA AAGGAGCTGA ATATACTCCT TTTACTGCAA AATATGCTCA AGCTGTTAAA
 TGGAGTGAAG CTTTTAAAC AGAATTACTG AAGGGAACCA AAGCTTCTGA TGAAACAG

EF094-4 (SEQ ID NO:360)

DEITH

PQEVTHYDV SKLYEVDGTF SDGSTLSEFT TSLYAEVHRA PQTVFCTIEP VSIPTEVTHG
 YQKNPLPSMS DKAKLVSVLW EKAGTI IDTN MVAQKMIWEE VNSYHLHSIK FLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKTLGQ STTLIDNHEL NLSEFNWVQ NTANIDYRVI
 GNQLVLTPTS NSKSGTLTLK KSAGTSTPVA YKPAQLTTH AGALENPNTY AIKINVETKG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

SLKIKKIDKE SGDIVPETVF HLDGFHALPS KMTTTHLFI SLLDTNHSI KMTTTEKSVP
 DPYMIETTPM AATIKAGETI SMTSKNMRQH SLLDTNHSI ETSTGNDN YSLAGNTFAI
 RKDSPAIEIV QEITTEKGR AETPKELANA LKSTTYNTE TRSTNHNNT FYPTKVELKY
 ANQTVALVTS NVKGCNQEIT GETTLTKEDF ETSTNHNNA EFTNNTLTF TANDSQAVKW
 SEAFKTELVK GTKASDET

EF095-1 (SEQ ID NO:361)

TAAGAATTGT TGGATTGTTT TTTAGAAAGA AGGTAATA TRLAGTGAAG TAAATGGAAA
 GAATTGATAG TAACGGGCAT CTGCCATATA TTATATTAC CCAATTAAT ACAGACAATT
 GTTTTGGCAG AAACATTACC AAGTACAAA CAAATTAAG AACGATCAA TCATTCACCTA
 ACAGCAGAAA AAGCCGAAAG TGAACAACCA CAGATTAAG ATAAATACA TGATGAAGAA
 ACACTGGCAT TGTCAAAAAG TGAGTTAATC CATATGAGC CTAATTTAC AAGTCAACG
 ATTAGAGAAA GAATTGAGAC GCTAACCTA ACTATTTT ATGATTTAT TAATGAAGAG
 GGGCAGCCAG TAAACGCCAA TGAGATCCTT CTACATATC ATAGTTGGA AGCAATTCC
 CCAGATGGCA TAAATGTGTG GBAAGGTGAA ACTATGAG TGATGATC TACAGTGGCT
 AATTTAAAAG AAGTGGTAAT TCCAAGTGA AATTAAGG TGTATGCGA CATGTCAACG
 GTGCTTGCG CGAGTAATCA AACATTTTTT TATCAAAAT ATTATCTTC TTTAAGCTTA
 TACAATAAGA AAGGGGAAAT TGATCCCAAT TATGCTTAC CAATATTTT CACGCGATCA
 GGAAACCAAT ATCCAACAAC AATTTGCAA TTTGATTTG AAAAAATGTC TGCACAACAA
 TATAGTCAGA AAACAGGAGT AACGTTTAA ATTAGGAGA GTCAAAAAC AATCGTTTCT
 TTGTACAACC AAGTGAAGGT TGATTCATCG AATCAATGT GGTATTTAA TTTACTTTAA
 TTTTCAGGCG CGGTTTATTA TCATGTTACC AATGCTTAC TGACAGAAC TTTTGTGGAT
 ACTCAAGGGA AACCAATCCC TCCACCACG GGGTTTACG AAGGAAAGCA AAGACTTATT
 GAGCGTGACC CTTACACCTT TAAACAGAAA GATTTTTCG CAATATCTA TGAATTTGAC
 TCAAAAACGT ATCAATTTCA AGGATGCTAT AATGCTTAA CCAATTTGA AATTTTAGAA
 AAAAGCGTAA CGCCAGTTA TGATATTACC TATGATGAA ATGATTTAT AACGTTTGT
 TATAAGGAGA TACCTCAAAA AAATTATACA TTTGATTTG TCAATGCTT TGAATTTGCA
 CCACCATCTG ATTTTATTTA GGATCACCAA CAATTTTAA CCAATTTGA CTTTGGCTAT
 TTAGCTGGAA AAAAACTGCG ACAACAATAC AGCTTTTAC GTAAAACTTA TTTATATCAA
 GGTGTTGATC AAGATAAAAC NAAACAAGAG AGCTTTTAA AAGGAAAGCG AACCATAAAC
 TCCCCTGTTT TTAATGAAAT GAACGCTATT ATAGCAAT ATAGGAAAT AACTGCAAAA
 GCTGAAATGC AAATAGAAGG ACTAGTCAA GTGATTTAA GTGTTTAT ACAAATTTGG
 CAGATTATGC TTACAAATGT GGGAGAAGTA GGTTTAAAA AATATAACTT AAAGCCAGCA
 AGTGGTTGGT CACCAGGTCT AGCTCGGCCA ATCCAGTCA CGATTGCTGT TGGATCTGAA
 CCAAAACAAA TTGTTCTTAT TACTGATGAA AATGCTTAC TTGGCATTAC TTTAAATACG
 GAAGTGCCTA TTGGTCAGAC AGCAACTATT ATGATGAGA CAATGCTAC AGGTGAACCA
 GATCAAGTGT TACAAGCGGC TGTGAAATG AATGCAATT TTTCTGCTGT TCACGCAGCT
 GATACTGTCA GAATCCAACC TAAAAATCAA AATTTTATG CACCATGTA GGAAGGTTTT
 ATCAGCACAC CAACTTTTGA TTTTGGCAAA GTGCTTATT CTAGCAACAC GCAGCAACAT
 GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGCTTAC AATTTTATA TTTACGTTTG
 AAAAAATCAC AACCAATTG GGCACAACT TGAAGATAT CCGCTTTGA AAGGAGAGTG
 GATCAACTAT CATCAATGAC AAAGTTATTG TTAGGAGAA CCAATTTTTC AGTTTATTAT
 CAGTACAATC AACCAACGGA AACTAAAGTT TTTTTTTAA AAACAACGCG TATTCAATTA
 GTTGGCAACG GTGTAGCTAG CCATATTGTT TCAATGCTC AATTTTACGA AAGTGTATGT
 TATCAATTTG ATTTTCTTT TGATCAAATC AATTTTAAA TTTGAGAAA TCAAGGTAGA
 AAAGATCAAA CTTATCAAGC AATGGTGACT TGAATTTAG TGACAGGCC ATAA

EF095-2 (SEQ ID NO:362)

MKRSKWKE LIVTGICHIL VFPILQTTV FAETIPSTK WREGNHOLT
 AEKAESQPP TKDKLHDEET LALSKSELID NEANTSTTI RERITPNTL YRYGFINEEG
 QPVNANEILL QYHSWQGNP DGINWEGES QPVTASTVAN LHEITPSEK VAVYSDMSTV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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LAASNQTFFL PRYYTSLSLY NKKGEIDPNY PLPTISDASG NQYPTTISQF ELEKMSAQQY
SQKTGVTFNI SESQKLIVPL YNQVKVDSSN QSGLELVHFP SGPVYVHVNTN RFVTEHFVDT
QGKPIPPPPG FRQ GKQTLIE RDPYTFKQKD LLMFVHIDS KTVDFGWYK GFTKPENLEK
SVTPSYDITY DDNDLLTVVY KEIPQKNYTF EDVNSVHIDP PSDFIQDHQQ PITTDGFRYL
AGKKLPPQYS VNGKTYLYQG WYQDKTKQES LEXHFFHHS PVFNEHIAIT AVYKEITAKA
EMQIEGLVKV MPSTGYIQIWQ IMLTNVGEVP LKKINLHFLS GWSPGLAPPI QVTIRVGSEP
NKIVPITDEN WRVGITLNT E VPIGQTATIM MTTIACGKPD QVLQAAVEMN GHFSAVHAAD
TVRIQPKNQ E IVAPDEEGFI STPTFDGKV AISSNTQCHG LKQADBYEN QQENPYLRLK
KSQPNWALTA ELSPFEGRVD QLSSMTKLLI GTTHVGFIDQ YNQPTETHYA LGKTTATQLV
ANGVASHIVA NGQFDES DVY QDFDSFDQIK LEIPANQGEK DQTYQAMVTV NIVTGP

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EF095-3 (SEQ ID NO:363)

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AAGTACAAAA CAAGTAAGAG AAGGAACCAA TCACTTATT.
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ACACTGGCAT TGTCAAAAAG TGAGTTAATC GATACAAAGS CTAACTTTAC AAGTCAAAACG
ATTAGAGAAA GAATTGAGAC GCCTAACCTA ACTTATCTTT ATGSAATTTAT TAATGAAGAG
GGGCAGCCAG TAAACGCCAA TGAGATCCTT CTACACTATT ATASTTGCCA AGGCAATTCC
CCAGATGGCA TAAATGTGTG GGAAGGTGAA AGTCAACGAS TGAACGATC TACAGTGGCT
AATTTAAAAAG AAGTGGTAAT TCCAAGTGAG AAAGTAGGGS TCTATTCCGA CATGTCAACG
GTGCTTGCAG CGAGTAATCA AACATTTTTT TTACCAAGAT ATTATACHTC TTTAAGCTTA
TACAATAAGA AAGGGGAAAT TGATCCCAAT TATFVSTAT CAACTATTTC CGACGCATCA
GGAAACCAAT ATCCAACAAC AATTTGCGAA TTTSATTTSS AAAAAATGTC TGCACAACAA
TATAGTCAGA AAACAGGAGT AACGTTTAAC ATTACGGA SA GTCAAAAAGT AATCGTTCCT
TTGTACAACC AAGTGAAGGT TGATTTCATCG AATTAATGTS GGTATTGSA TACTTTTAAA
TTTTTCAGGC CGGTTTATTA TCATGTTACC AATTCGAAS TCAAGAAACA TTTTGTGGAT
ACTCAAGGGA AACCAATCCC TCCACCACCG GGGTTTAAT AAGSAAAGCA AACACTTATT
GAGCGTGACC CTTACACCTT TAAACAGAAA GATTTTTTSS CAAGTAGCTA TGAAATTGAC
TCAAAAACGT ATCAATTTCA AGGATGGTAT AAAAGGAAA CGAAAGCTGA AAATTTAGAA
AAAAGCGTAA CGCCAGTTA TGATATTACC TATACGGA ATGATGATTT AACTGTGTGTC
TATAAGGAGA TACCTCAAAA AAATTATACA TTTAGGATB TCAATGSTST TGAAATGCA
CCACCATCTG ATTTTATTCA GGATCACCAA TAACCAATA CTACGGATG CTTTCGCTAT
TTAGCTGGAA AAAAAGTCC ACAACAATAC AGCCTTAATB GTAAAACTTA TTTATATCAA
GGTTGGTATC AAGATAAAAC NAAACAAGAG AGCTTAGAAA AAACGAAGCG ACCCATAAAC
TCCCCTGTTT TTAATGAAAT GAACGCTATT ACAGCACTST ATAAGSAAAT AACTGCAAAA
GCTGAAATGC AAATAGAAGG ACTAGTCAAA STCATGSAHA GTGTTTATAT ACAAATTTGG
CAGATTATGC TTACAAATGT GGGAGAAGTA CCGTTAAAAA AATATACCTT AAAGCCAGCA
AGTGGTTGGT CACCAGGTCT AGCTCGGCCA ATCCAACTTA CGATTGCTST TGATCTGAA
CCAAACAAAA TTGTTCTTAT TACTGATGAA AATTSSTGAS TTGCTATTAC TTTAATACG
GAAGTGCCTA TTGGTCAGAC AGCAACTATT ATGATGAGAA CAATTSTTAC AGGTGAACCA
GATCAAGTGT TACAAGCGGC TGTGAAATG AATGSAATTT TTTCTGCTST TCACGCAGCT
GATACTGTCA GAATCCAACC TAAAAATCAA GAAATGCTSG CACGAGATSA GSAAGGTTTT
ATCAGCACAC CAACTTTTGA TTTTGGCAAA STCCCTCTTT STAGCAACAC GCAGCAACAT
GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGSTGAGS AAAATCATA TTTACGTTTG
AAAAAATCAC AACCCAATTG GGCACATACT GCAGAACTAT CCGCTTTTSA ASGAAGAGTG
GATCAACTAT CATCAATGAC AAAGTTATTG TTASBAACAA CCAATGTTTC AGGTTTTATT
CAGTACAATC AACCAACGGA AACTAAAGTT GCTCTTGCCA AAACAACGSC TATTCAATTA
GTTGCCAACG GTGTAGCTAG CCATATTGTT GCGAATGCTC AGTTTGACSA AAGTGATGTT
TATCAATTG ATTTTCTTT TGATCAAATC AAATTAAGAA TTCCAGCAAA TCAAGGTAGA
AAAGATCAA CTTATCAAGC AATGCTGACT TCGAATTTAG TCACAGGCCC A

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EF095-4 (SEQ ID NO:364)

STKQ VREGTNHSLT

TABLE 1. Nucleotide and Amino Acid Sequences of *Helicoverpa* Genes.

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AEKAESEQCFE TWKHLDEET LALSKSELIF SHATG LLI HIAITINLT VRYGFINEEG
QFVWANEILL QYHSWQGNSE DGINWMESEF THTG LLI HIAITINLT VRYGFINEEG
LAASNQTFEL PRYYTSLSLY NKKCEIDPNT ELIET LLI HIAITINLT VRYGFINEEG
SQKTGVTFTNI SESQKLINFL YNQKVDSSN LALSKSELIF SHATG LLI HIAITINLT VRYGFINEEG
QGGPIPPFPB FRQCKTLIE ADPYTFKQKE LLI HIAITINLT VRYGFINEEG
SWPSPYDITY DNDDELITVY KEIPQKNYTF ELIET LLI HIAITINLT VRYGFINEEG
AGSKLPQQYS VNGKTYLYQS WYQDXTQES LLI HIAITINLT VRYGFINEEG
EMQIEGLWVY MFSGYIQIWQ IMLTNGENF LLI HIAITINLT VRYGFINEEG
NKIVPITDNF WVGITLNTF VPIBQTATIM LLI HIAITINLT VRYGFINEEG
TVRIQPKNQE IVAPDEEGFI STPTFDESKV LLI HIAITINLT VRYGFINEEG
KSQPNWALTA ELSPFEGRVD QLSMTKOLL LLI HIAITINLT VRYGFINEEG
ANGVASHIVA NGQFDESDVY QFDFSPDQIR LLI HIAITINLT VRYGFINEEG

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EF096-1 (SEQ ID NO:365)

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TGAGGTGGCC AAGTTAAAT GAAAAAATTA GATGCTCTT TATGCTGAT TATGCTGAT
ATTGCTCATCT TCTTTTCTG GGTGCGGCAA TGTGCTGAT TATGCTGAT TATGCTGAT
GATACCTTGA CCATTACAA TTGCGGGGAC TATGCTGAT TATGCTGAT TATGCTGAT
GAAAAAGAAA CAGGCTATAA AGTCAATTAC GATGCTCTT TATGCTGAT TATGCTGAT
ACAAAAATTC AGCAAGGTGG CACAGCCTAT GATGCTCTT TATGCTGAT TATGCTGAT
CAAAAAATGA TGAAAGCGAA CATGCTTTTA TATGCTCTT TATGCTGAT TATGCTGAT
GAAAAACATT ATGCACGCTT TTTAGATCAA TATGCTCTT TATGCTGAT TATGCTGAT
CGGTACTTCT GGGGCACGTT GGGGATTATT TATGCTCTT TATGCTGAT TATGCTGAT
ATGCAACATT GGGATGATTT ATGCGCGCCS GATGCTCTT TATGCTGAT TATGCTGAT
GGCGCTCGCS AAGTGTAGG ATTATCTTTC AATGCTCTT TATGCTGAT TATGCTGAT
AAGGACCAAC AATTACGTA GGCTACCGAT AATGCTCTT TATGCTGAT TATGCTGAT
GCAATTGTTT CCGATGAAAT CAAAATGTAC ATGCTCTT TATGCTGAT TATGCTGAT
ACTTTCTCTG GTGAAGCTGC TGAAATGCTA GATGCTCTT TATGCTGAT TATGCTGAT
CCCTGCTAAG GCTCTAATCT CTGGTTTGAAT AATGCTCTT TATGCTGAT TATGCTGAT
AAAGAGGGTG CCTATGCATT TATGAACCTT AATGCTCTT TATGCTGAT TATGCTGAT
GCAGAATATA TTGGTTATTC CACACCAAAT AATGCTCTT TATGCTGAT TATGCTGAT
GTTCGCCAAG ATAAACAATT TTATCCAGAT GATGCTCTT TATGCTGAT TATGCTGAT
CAAGACTTAG GTCAAGAATA CTTAGGAATT TATGCTCTT TATGCTGAT TATGCTGAT
TATCGGAAAT AA

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EF096-2 (SEQ ID NO:366)

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MKKLQ SLFIGIIAI VILFFGVRQL EKASGMAGAG LLIYNGGV ICPALIKKFE
KETGYKVNYE TFDSEAMYT KIQQGGTAYD IATGCTCTT TATGCTGAT TATGCTGAT
NIDARFLDQS FDPFNKFSVP YFWGTGLIY NKKCEIDPNT ELIET LLI HIAITINLT VRYGFINEEG
AREVLGLSLN SLGYSLSKN DQQLRQATDK LLI HIAITINLT VRYGFINEEG
FSGEAAEMLE NNEHLHYVIP SEGSLWFDN LLI HIAITINLT VRYGFINEEG
EYIGYSTPNK EAKHLLPKVE AEDKQFYPPD LLI HIAITINLT VRYGFINEEG
RK

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EF096-3 (SEQ ID NO:367)

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AAGTGGCAT GGCAGGAGCA
GATACCTTGA CCATTACAA TTGCGGGGAC TATGCTGAT TATGCTGAT TATGCTGAT
GAAAAAGAAA CAGGCTATAA AGTCAATTAC GATGCTCTT TATGCTGAT TATGCTGAT
ACAAAAATTC AGCAAGGTGG CACAGCCTAT GATGCTCTT TATGCTGAT TATGCTGAT
CAAAAAATGA TGAAAGCGAA CATGCTTTTA TATGCTCTT TATGCTGAT TATGCTGAT
GAAAAACATT ATGCACGCTT TTTAGATCAA TATGCTCTT TATGCTGAT TATGCTGAT
CGGTACTTCT GGGGCACGTT GGGGATTATT TATGCTCTT TATGCTGAT TATGCTGAT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATCCAACATT GGGATGATTT ATGGCGCCCC GANTTAATAA ATAATATCAT GCTGATTGAT
 GGCCTCGCG AAGTGTAGG ATTATCTTTG AACATTTAG GCTATCGTT AAACAGTAAA
 AACGACCAAC AATTACGTCA GGCTACCGAT AACTTAATAA GATTACGAA CAATGTCAAA
 GCAATTGTTG CCGATGAAAT CAAAATGTAC ATGGCTAATA AAGAAAGTSC AGTTGCTGTA
 ACTTTCTCTG GTGAAGCTGC TGAAATGCTA GAAAACAAA AACATTTAAT TTATGTGATT
 CCCACTGAAG GCTCTAATCT CTGGTTTGAT AACATTTCTA TGGCTAAGAC AGCCAAAAAT
 AAAGAGGGTG CCTATGCATT TATGAACCTT ATGTTACCA CAGAAAAATG GGCACAAAAAT
 GCAGAAATATA TTGTTTATTC CACACCAAAT AAGAAAGTAA AAAAACTATT ACCAAAAGAA
 GTTGCCGAAG ATAAACAATT TTATCCAGAT GATGAAATTA TTAACATTT AGAAGTTTAC
 CAAGACTTAG GTCAAGAATA CTTAGGAATT TATTAAGATT TGTCTTTTAA GTTTAAGATG
 TATCGGAAA

EF096-4 (SEQ ID NO:368)

SGMAGAD TLTIYNWGDY IDPALIKKFE

KETGYKVNYE TFDSNEAMYT KIQQGGTAYD IAIPTKWTY KMKRHHILP LDHSLKLGLE
 NIDARFLDQS FDPKNKFSVP YFWGTGLIY NDRILDTY QWDELWRPE LFNVMMLIDG
 AREVLGLSLN SLGYSLNSKN DQQLRQATDK LNELTNWNL IVADEIKMYM ANEESAVAVT
 FSGEAAEMLE NNEHLHYVIP SEGSNLWFDN IYKPEHNNK EDAVAEINFM LEPENAAQNA
 EYIGYSTPNK EAKKLLPKEV AEDKQFYPDD ETTRHLLTP DLGQETNGIY NDLFLEFKMY
 RK

EF097-1 (SEQ ID NO:369)

TAGAAGTATT CTAATTATCT ACATAGAGAG CGATGSAATA GANTATPAA GAAAAAGAA
 ATGCATTCGC TCTTTTTTAA ACATAAGTTT GTGAAGTAA CTTCCTAATT AGTCGTTTTT
 GGTATCGTT TGAGTGGGAT GATTATGCCA AATTGSAATA TTTTMTTSC CTGGAGCTTA
 TTGTCTTTG TGGCTGGCTA TACGACTGGG AATTATATCT TAGCTCTTTC TBAAGTCGAA
 ACGATAATGA TTCGAGTTGT TTTACCGATT CTATTGCTT TIACAGSDGG AAAAAATGTTT
 GAGGAACAAC GTGGCGGCGT TGTTCGTGCT ATTGCGAATA TGGGCTGAT TGTTCACACA
 GATGTTCCAC AGTTGTTTGG TGCTATGTTT ATTGCGCTT TAGAGGATA TACTTTCGCC
 AAAATTGAAC AAATTCTCTT ACCGAAAGTT AAGAAAGCT ADBAATGCT GACTAAAAAC
 TTTTATAGCAG GAATTGTGGG AGGACTGCTG TGCCTTTT GATTCTTST T3TAGCTCCG
 GCTGTTGAAA GCGCTAGTTT TTGGCTGTAT CAATTCTCTT CTGCTTAAT TBAAGCCAAT
 CTTTACCAT TGGTTCACGT TTTCTTAGAG CCCTTAAGG TSTATTITTT TAATAATGCC
 ATTAACCAT GCTTATTAAC GCCTCTAGGT TTAAAGCTB CTACTCAAC AGGTCAGTCC
 ATTTTATTTT TATTGGAAC AAACCCTGGA CCAGGCTGA G3TTTIGST T3CTTTTCTG
 CTGTTTGGGC CTGTAGGACA ACGAAAAACA GCAGGASIB CDACCATGAT TCAACTGATT
 GGGGGCATTC ATGAAATTTA TTTTCCGTTT GTTTCATIB A3CGT3CTT ATTTTATAGCA
 GTAATTGCTG GAGGAATGAG TGGTACGCTT GTTTCATGA TATTTAATGT G3GTCTAAGT
 GCTCCAGCTT CGCCAGGTTC ATTGGTTGCG ATTTTASIA AT3CCCTCAC T3ATGCGAGG
 CTGGCGGTTT TTAGCGGAAT TTTTGTAGC TTTCTGTCT CTTTTCAAT A3CAAGCTTG
 TTATTAACAAC GTCAACGAGG AATTGAACCA GTTTCATTA TAAAGATGAA GGAGGAAGAC
 CAAGTGGAAA CAGTCACACC TAACTATCAG CAATTTTAT TTSTTTTGA TGCAGGAATG
 GGCTCAAGTG CCATGGGGG TAGTTTGCTA AG3CGAAT TAAAAGTGT GAACCTGGAG
 ATGCCCTGTGA CTTACCATC CGTTCATCAG AT3AGTCTC AGCCTAAGAC ATTAGTGGTC
 ATTCAAGCAG AATTGAAACA GTTAGCACAA AASTACCTC CAGAAAAGGA TATGGTGAGT
 GTTCAAAATT TTTTAGAAAT TAAATCTAT TATCGAAB TTTTAGTAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGGTTCA GAPTCTACB AAGCGAATC GACAAAACAA
 ATACAGAAGC TTGTTTTTTT ATATGCCGAG AATCTTCTB GATGGAAC AATGGGAATG
 GAATTATTGC GGCAACAAGC GGCGAAACAA GGACTCTCA T3CAATATC TAAAGAGCCA
 CTGGAAACAG TCTTTTTTAC CAAGGAGACA ACCTACCTG T3ACTT3TGA ACTGGCGCAA
 GCCTATCATT TAGATCTAAC GCAACAAAAT TTATCTTAG TTACTT3TTT TTTGAATAAG
 AAAGAGTATC AAGAATGGCT GGAAGGAGGA GCTGATATAT TTTTITTA

TABLE 1. Nucleotide and Amino Acid Sequences of *Phaeo* Genes

EF097-2 (SEQ ID NO: 970)

[illegible]

EF097-3 (SEQ ID NO:371)

ACGAGG AATTGAACCA GTTTCATGTA TAAAGTAA TAAAGAAA
CAAGTGGAAA CAGTACACCC TAACATATCA GAAATTTAT TCGTTTGTGA TCGAAGAATG
GGGTAAAGTG CCATGGGGGC TAGTTTCTCA AATCAAAAT TAAATTTGT GACTTTGGAG
ATGCTGTGTGA CTTACAGTCG CGTTTCATCA AATCAAAAT AACTTAAGAG ATTAGTGGTC
ATTCAAGCAGC AATTGAAACA GTTATACAGA AACTAGTTC CAGAAATAGA TATGTTGAGT
GTGCAAAATT TTTTAGAAAT TAAATCTAT TAAATTAAG TTTTAAAGAA AATGACTGCT
TCTTCTCAAG AGCAATCTTC ACTTCTTCA GACTTATCT AAAGCAATTC GACAAAACAA
ATACAGAAGC TTGTTTTTTT ATATCCCGAG AATCTTCA GATCTAAAG AATGGAATG
GAATTATTGC GGCACAAGC GGCGAAACAA GCATTTTCA TTAATTTATC TAAAGAGCCA
CTGAAACAGC TCTTTTTTAC CAAGAGACGA AACTATTTAG TCAATTTTGA ACTGCGCGAA
GCTATCATTT TAGATTTAAC GCAGAAAAAT TTATATTTG TTAATTTTCT TTTGAATAAG
AAGAGTATC AAGAAATGGCT GGAAAGAGGA GCTATTTCT GATTTTCT

EF097-4 (SEQ ID NO:372)

RGIEPV SMIKMKEEDQ VETVTPNYDQ ILFVGTASIN VAMGASILL RQKRAHILEM
PVTVQSVHQM KWQPKTLWVI QAEKQLAQK YVWHTHTYV QHTLEIRSVY PQVLAKLTAS
SQEQSSLGSE STETNSTKCI QKLVLFLYAEH VEGVYTHWE LLRTAAHQB VAIEVSKEPL
ETVEFTKETT YVVTRELACA YHLDLTOCNL YVWTFEINHE EYENLEGA DRDF

EF098-1 (SEQ ID NC:373)

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CTTGTAACCA	TGAGTGCATT	AGCASTCGAC	GCTGTTGAAAT	ACGAAAGCAA	CGGAGCGATT
CAATTTGCAC	CAAATACGAA	CCCAACGAAT	CGASTTCAATG	CGAGGAATCG	AGACCCAGAT
AAACCAATTA	CACCAGTTGA	TCCAACTEAT	CTGAAAGGTC	CTAAGCCAGG	GACAGCAGGT
CCGTTATCCA	TTGACTATGC	ATCTAGCTTA	TCTTTCTTTC	AAGCAAGCAT	TACCTCAAAA
AATATGACCT	ACTATTGCAG	AACACAAAAA	TACAAAAATA	ACGGTGTGTG	CGCCCAAGAA
GGCCCCAACT	TTGTTCAAGT	CTCAGATAAT	CGTCTGACTG	AGACAGGTTG	GAAGCTAAAA
GTAAAACAAA	ATGGTCAATT	CAAAACAGAA	GTCAATCTTG	AAGTATACAG	GGCCAAAGTA
ACTTTAAGCA	ACGGACGCGT	GGTTTTCAGCT	TCACAACTTG	CAAGGCGAAG	GACAGCGCCA
GCTACGATTG	AATTAACCCC	AAC TGCGGCT	GAATATCTTG	TTATGCGTTC	TGCGGATAAA
GAAGGCTCAG	GTACGTACTT	AATGAGCTTG	GGGATATATG	TAGATACCGC	TAAAACAAGT
ATTTTCATTG	AAGTACCTGT	TTCAACCCGA	AAATATCTTA	AAAAATTCAG	GACAACTTTT
ACTTGGACTT	TGACAGATAC	ACCTGCTAAC	ACGGGAGGCT	AA	

EF098-2 (SEO ID NO:374)

MKKTKVMTLM ATTLPLGALAL VPMSALAVDG GENTHEDKQ FAKHTNNTNP VQPTNPDPDK
 PITVPDPTDP TGPKPGTAGP LSIDYASSLS FSEKIDTNN KNTYAEKTKY EDNAGADQEG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PNFVQVSDNR GTETGWLKV KQNGQFKTEA NHEITAAKVT LSNGRVVSAS QSAKPPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DEVDTPANTSI SLEVDSTTK YAKKYTTTTFT
 WTLTDTPANT GN

EF098-3 (SEQ ID NO:375)

AGTCGAC GGTGGTGAAT ACCAAACAAA CGGAGCGATT
 CAATTTGCAC CAAATACGAA CCCAACGAAT CCATTTGATC CGACGATATCC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAACGTAT CCGATAGGAC CTAAGCCAGG GACAGCAGGT
 CCGTTATCCA TTGACTATGC ATCTAGCTTA TTTTCTGCTG AACAAACGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAAA TACAAATATA ATGCTTSTGC CGACCAAGAA
 GGCCCAAACT TTGTTCAAGT CTCAGATAAT CTTTACGCTG AGACAGSTTG GACGCTAAAA
 GTAAAACAAA ATGGTCAATT CAAAACGAA CTTTACGCTG AACTATCAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GGTTCAGCT TTTTACGCTG CAAAGCCAAAC GACAGCGCCA
 GCTACGATTG AATTAAACCC AACTGGGGCT GATATGCTG TATGCTTGC TGGCGATAAA
 GAAGGTGCGG GTACGTACTT AATGAGCTGG SLEVDSTTK TACATATGCG TAAAACAAGT
 ATTTTCATTAG AAGTACCTGG TTCAACCACA AATATGCTG AATATACAC GACAACTTTT
 ACTTGGACTT TGACAGATAC ACCTGCTAAC AATGAAACT

EF098-4 (SEQ ID NO:376)

VDG GEYQTNQAIQ FAPNTNPTNP VDPNTNPDPE
 PITPVDPTDP TGPKPGTAGP LSIDYASSLS FHEHTITSEN MITYAETQKY KDNAGADQEG
 PNFVQVSDNR GTETGWLKV KQNGQFKTEA NHEITAAKVT LSNGRVVSAS QSAKPPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DEVDTPANTSI SLEVDSTTK YAKKYTTTTFT
 WTLTDTPANT GN

EF099-1 (SEQ ID NO:377)

TGATGTTGTA GAGGGCTGAT GAAATGTTTA TTAATGTTTA TTTTATGAA AGGAGAGATC
 ATGAAGAAAT TAGGCAAGGT TTTAATTGTT ATTGTTTGA TTTTATGCT TCTTTTTTA
 TTATTTTTAG GTGATTTTTT TTCTAGTGAA AATGAGGATT CTTCAGATT TTAGCCCGCT
 ACACCACAGG AAAAAGTAGC ATTAGAAGTT TTTAATGAG TGACGTCACA TGGCGGAACG
 TTGCAGTTTG CTTCGCTTG GATTGGCAAT ATGGAACATG AAAGTGCAAT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATTCA GATATGCTT TTAATGCTT GTTAGGCGGT
 TATGGAATTG GGTAGGACA ATGGGATTCA GAGGAGAGG TTAATTTATT AAATTTGCA
 AAAAGTCAAA AAAAGGAATG GAAATCAGTA GATTTACAAA TGSATTTTG GTGGAATAAG
 GATGTTCTG ATAGTGACTT ACTTAAAAGA ATGTTTAAT CAAAAGATGT GAATACACTT
 GCGGTAGATA TTTGAAGCT GTGGGAACGA GGTGGAACAA AAGATATCC CGCAGAACAA
 GTAAAAAGAA AGGCTAGTGC TAATAATTGG TATTAATGAC TTTTACAGG TTCCATGGGC
 GGAGGTTTCA CCAATGTTGG TGGAGGAAAA ATTGATGCTT TGAAGAAAGT GATGGGCAA
 ACTATTAATG GTGTCAATG TTATGGCTTA TCTGCTTFT TTTTCAAAA ACAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GCGASTHAAA TTGTAATGA TTATCCTTGG
 AGTTCAATTG GTTGGACAGT CATAAAGAAT CCAATTTATT CAGATATTAA AGCAGGAGAT
 GTCATTAATT TTGGTCAAGG TGGTGTGGCT ACTATATTT ATGCGCATAC TGGTGTAGTG
 GCAAGTGTG AAGGTAAAAA CAAGTTTACT ACTATGAGC AAAACGGTGA ACAAGGTCAA
 ATTGTTGCTA AGTATTTTCG GACTTGGGGA TTATTTTTC CACATGTGAC CAGCATAGTA
 AGGAAATAG

EF099-2 (SEQ ID NO:378)

MKCLS VFLLKGEIM KKLGVLIIV CFIFILFFIL ELNVFSSSES GDSQFQPAT
 PQEKVALEVS NYVTSHGGTL QFASAWIGNM EHESULNPAR IQDLSTNSA IAFNPSLGGY
 GIGLGQWDSG RRVNLLNFAK SQKKEKWSVA LQMTFARNED GDSSELNRM SKSKDVNTLA

TABLE 1. Nucleotide and Amino Acid Sequences of the Invention Genes.

VDILKLWERA GTFDPAEQV KKKASANTWY FHLK...
 INGGQCYGLS AFFVEKQGL QMMGTGHNFA...
 INFGQGGVAT SIYGHTGVVA SVEKKNKFTT...
 K

EF099-3 (SEQ ID NO:379)

TAGTGAA AGCGAGATT GTTCCCACTT TCAG...
 ACACCACAGS AAAAAGTAC ATTAGAACTT...
 TTGACGTTT GTTCCGCTTG GATTGGCAAT...
 AGAATTCAAA GTGATTTATC GTTTAATTC...
 TATGGAATTG GTTTAGGACA ATGGGATTC...
 AAAAGTCAAA AAAAGGAATG GAAATGACT...
 GATGTTCTG ATAGTGACTT ACTTAAAGA...
 GGGGTAGATA TTTTGAAGT GTTGGAAAG...
 GTAAAAAGAA AGTTTAGTTC TAATAATTG...
 GAGGTTTCAG CCAATGTTT TGGAGGAAA...
 ACTATTAAAG GTTGTCAATG TTATGGCTA...
 CTACAAATGA TGGGTACGGG GCATATGTT...
 AGTTCAATTG GTTGGACAST CATAAAGAT...
 GTCATTAAAT TTGTTCAAGG TGGTGTGCT...
 GCAAGTGTG AAGGTAAAAA CAAGTTTACT...
 ATTGTGCTA AGTATTTTCG GACTTGGGA...
 AGGAAAT

EF099-4 (SEQ ID NO:380)

SES GDSSQFPAT
 PQEKVALEVS NYVTSHSGTL QFASAWIGIZ...
 GIGLGQWDSG RRVNLLNFAK SQKKEKNSVA...
 VDILKLWERA GTKDDPAEQV KKKASANTWY...
 INGGQCYGLS AFFVEKQGL QMMGTGHNFA...
 INFGQGGVAT SIYGHTGVVA SVEKKNKFTT...
 K

EF100-1 (SEQ ID NO:381)

TANTTATGGC AATATGGAAG GAGTTTATA...
 ACATTATTAG AAATGTTGAT TGTCTTATTG...
 CCTAAGTTAG CGAAACATAA AGAAACAGTT...
 ATTGTAGAAT CACAAATCGA GCTCTACACA...
 GAATTAGTCA ACGAAGGCTA CATTACTAAA...
 CAATGA

EF100-2 (SEQ ID NO:382)

MKKKQKYAGF TLEMLIVLL IISVLILLFV...
 IVESQIELYT LEKNKTPSLN ELVNEGYITK...
 EQLLVTADEK

EF100-3 (SEQ ID NO:383)

TAA AGAAACAGTT GATAAAAAAG GCAATGA...
 ATTGTAGAAT CACAAATCGA GCTCTACACA...
 GAATTAGTCA ACGAAGGCTA CATTACTAAA...
 AGCAGAAAAAG

10

TABLE 1. Nucleotide and Amino Acid Sequences of *C. faecalis* Genes.

CAAT

EF100-4 (SEQ ID NO:384)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLEHYTAER Q

EF100-1 (SEQ ID NO:385)

TANTTATGGC AATATGGAAG GAGTTTTATA ATGTTTACA AACAAAAATA CGCAGGGTTT
 ACATTATTAG AAATGTTGAT TGTCTTATTC ATTATTTCG TATTGATTTT ACTTTTTGTC
 CCTAACTTAG CGAAACATAA AGAAACAGTT GATGAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGAGCGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCATTAG ATAALTATAC AGCAGAAAAAG
 CAATGA

EF100-2 (SEQ ID NO:386)

MKKKQKYAGF TLLEMLIVLL IISVLILLFV PNLANNHEETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLEHYTAER Q

EF100-3 (SEQ ID NO:387)

TAA AGAAACAGTT GATAAAAAAG GCAATGAAGT ATTGCTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGAGCGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCATTAG ATAALTATAC AGCAGAAAAAG
 CAAT

EF100-4 (SEQ ID NO:388)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLEHYTAER Q

EF101-1 (SEQ ID NO:389)

TGAGGAGATG AAACGAAGAA AATGAAGAA AAAATGATTA TTATATTGGG GGCAGTTGCG
 GTAATTGCGG TTGGGGGCAT CGTAACTGTG AATGCTTAA ATAAAAATGC ACAACAAGTA
 GCTGTCAAGC AAGCGCCTAA AGATGACTGG GGAATTACT ATTTTGACBT TCCCGACTTG
 CAACAAATTT ATATTAACGG TGTATCCAA CCGGAAATA TGGAAAGCCTT TCGCGGTGAT
 CAAAAAATAA CAAAGGATCC AGAGATTAA GTGAAAGAG GCGATGTCT AGATGCAGGC
 ACAGAATTAT TTACTTATGA AGATGAGGCG GTCAAAAAAG AAATTGAGGC ACAACAAAAT
 AGCTTAGCCA AATTAGAAAC GAAGCGGGCG AATATCTATA ATAAGTGGAA TCGGGCCATT
 GATAAATTTA ATAAACTAA AGAAGAAGT CCGAATCTCT CTGGTGATGA TTTAAATGAA
 CAATATCAAA CAGAAGTCGA TGCAGTAGAT GAAGAAATA CCTTCACCAA TGAAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTC AGAAATCTA ATTTGAAAG TCGTGATATCA
 ATTCCAGAAG TAAAAGATGC CAATTCACCG ATTTGATGCT TAATTTGASA AGATCTTTAT
 TTAGCTGGAA AAGTGAATGA AAAGGACTTG ACTAATATTA GTGTGGGCA AAAAGCTAAA
 CTAATTCTGT TTTCCAACAA TGTGGTTGTG GATGCTTCA TTTCTTACAT CGATGATAAT
 CCTCTGAAG GCAACAGCGA TGCCGCGAGT GGCATTTAG AGGCGGGCAC AACGATGTCT
 AGTTATAGCG TCAAAATTGC GTTGGCCAAT TTAGAAAGG TCAAAAATGG CTACCATATG
 CAAGCAACCA TTGATTTAGG CGATTTAGG GCGATTTAGT TACCGAAAAA AGCGATTCAA
 AAAGAGGGTG AACAGGCCTA CGTTTTAGTG AATGATTTG GAACCATCAT TCGTCGTGAT
 GTCCAAGTCG GGCAAGAAAA TGGCGACAAA ATGCGGATTC AATCTGGCTT AGAATCAGCC
 GACCGAGTGG TTATTTCTTC AAAAAACCA GTAAATTTCT GTGATATTGT TSAATCAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of the Genes.

GCAGCGATTG CTTCTGATGA ATCAGCAACG AATTG TAA TATTATATCC GTTGAAATAG

EF101-2 (SEQ ID NO:390)

MEKK TIIILGAVAV IANGSINTN ALINNAQ, Q TALKHNG IUNEDVPL,
 QIYINGVIQP EQMEAFARD; KITKDPEIKV KNGDNHAGT ELFTYEDEAV TREIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEEDR TMSGGLNEF YQTEVDANDE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LELTGLDLVL AGHWNKELT KISVQKAKL
 TSVSNNVVVD GSISYIDNP PEGNSDAASG NPEGGTMSF YSVKIALANL DKVKNGYHMQ
 ATIDLGLDGA IELPKKAIQK EGEQAYVLVN DFETLHNEF QVAGLNGNEM AIESBLESAD
 RVVSSKKPV KVGDIVESDA AIASDESATN ESHTLAFV

EF101-3 (SEQ ID NO:391)

TAAAAATGC ACAACAAGTA
 GCTGTCAAGC AAGCGCCTAA ABATGACTGG GAAATGAGT AATTGAGGT TCCGACTTG
 CAACAAATTT ATATTAACGG TGTGATCCAA GTGAGTAA TGGAAAGCTT TCCGCGTGAT
 CAAAAAATAA CAAAGGATCC ABAGATTAAG GTGAGTAA TGGAAAGCTT AGATGCAGGC
 ACAGAATTAT TACTTATBA ABATGAGGCG GTGAGTAA TGGAAAGCTT ACACAAAAT
 AGCTTAGCCA AATTAGAAAC GAAAGCGGCG AATTGAGT AATTGAGGT TCCGCGCATT
 GATAAATTTA ATAAAACTAA ABAAGAAGAT TCGAGTAA CTGGGATGA TTTAAATGAA
 CAATATCAAA CABAAGTCBA TCGAGTAA TCGAGTAA TCGAGTAA TCGAGTAA
 GCGGATTTAG GAGCGAAGCA ATATATTTTC ACAAAGCTA AATTGAGGT TCGGATGA
 ATTCGAGAAG TAAAAGATGC CAATTCAGCG AATTGAGT AATTGAGGT TCGGATGA
 TTAGCTGGAA AASTGAATBA AAAAGGACTG ACTAGGCTA GTTGTGCGA AAAAGCTAAA
 CTAAGTTCTG TTTCCAACAA TGTGCTTGTG GATGAGTAA TTTGATCAT CAGTGAAT
 CCTCCTGAAG GCAACAGCGA TCGCGGAGT GCGAGTAA AGGCGGCGAC AAGGATGTCT
 AGTTATAGCG TCAAAATTTC GTTGGGCAAT TTAGAAGAG TCAAAAGCTG CTAGCATATG
 CAAGCAACCA TTGATTTABG CBATTTAGBG GCGTAAAGT TACCGAAGAA AGGATTCAG
 AAAGAGGGTG AACAGGCCTA CSTTTTAGTG AATGAGTAA GAAGCATGAT TCGTGTGAT
 GTCCAAGTCG GGCAAGAAAA TCGCGAAGAA AATGAGTAA AATGAGTAA AATGAGTAA
 GACCGAGTGG TTATTTCTTC AAAAAAACCA GATGAGTAA GTGATATCTT TGAATCAGAT
 GCAGCGATTG CTTCTGATGA ATCAGCAACG AATTGAGT TCGAGTAA GTCGAAAT

EF101-4 (SEQ ID NO:392)

KNAQQVA VKQAPKDDWG IDYFVDPDLQ
 QIYINGVIQP EQMEAFARDQ KITKDPEIKV KNGDNHAGT ELFTYEDEAV TREIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEEDR TMSGGLNEF YQTEVDANDE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LELTGLDLVL AGHWNKELT KISVQKAKL
 TSVSNNVVVD GSISYIDNP PEGNSDAASG NPEGGTMSF YSVKIALANL DKVKNGYHMQ
 ATIDLGLDGA IELPKKAIQK EGEQAYVLVN DFETLHNEF QVAGLNGNEM AIESBLESAD
 RVVSSKKPV KVGDIVESDA AIASDESATN ESHTLAFV

EF102-1 (SEQ ID NO:393)

TAAACATTTG AGACATTCAG AGGTGAATBT CTGTTTATTA TTAGTCAAAA ACCGAAAGGGG
 ATTAATTATA TGAAAAAAC AACATTTAAA AATTGAGT TATTGCGAC TTTGCTCTA
 TTAAGTCAAA CAATTGGCGG AACGATTGCT CCTAGATTT CTGTTGCGCA TGAAATTACT
 CACCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAG TGTATGAAGT TGACGGAAGT
 TTTAGCGATG GCAGCAGCT CTCAGAACCT ACTAGTCAAT TATATGCAGA ATACAATGGT
 GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTGCAACAGA AGTGACGCAC
 GGTATTCAGA AAAACCTTT GCCATCAATG TGTGATAAAG CGAAAGTACT ATCGSTTCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATATTT CACAAAAGAT GATTGCGAA
 GAAGTGAACG GTTATAAACT CCATTCCATA AAAAAAGT GTGTTGCTTC AGTTGATATA

TABLE 1. Nucleotide and Amino Acid Sequences of *Trichoplax* Genes.

AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGA - GAT ATGAAAAAAA ACCAAGTTT
 CATAATACCA CTGTAAAAAC AATTTTAGGT CATTGATGAA CTTTAATAGA TAAAAATGAA
 TTAAATTTAT CTGAGTTTGA TAAAGTCGTC CAAATATGAG CGAATATAGA TTACCGTGTA
 ATTTGGGAATC AATTAGTGCT TACTCCAAAC TCTAAATGCA AATCAGGAAC ATTAACATTG
 AAAAAATCAG CTGGTACTGG AACTCCAGTC GTTATATGAA AAGCAGGACT TCAAACGTG
 ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTTTTA AATTAATGAT GGAAACTAAG
 GGTTCTTTAA AGATCAAAAA AATCGATAAA GAATCGAGTG ATATGATAC AGAAACGGTT
 TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAGATATG TGACAAACAGA TAAAGATGGG
 ATTTCTATTT TGGATGGAAT TCCCCATGGT ADAAATATTA CTATTACTTA AAAATCGGTG
 CCAGATCCTT ATATGATTGA TACCACACCC ATGCTTATTA CATTAAAGC GGGCGAGACC
 ATTTCCATGA CTTGCAAAAA TATGCGACAA AAGGCAAAA TTCTTTTGA GAAGACTGGG
 GTAGAAACAG GTACTGATCT TTGGAATGAC AATTAATGCT TACCTGGGAA TACATTTGCC
 ATTCGTAAAG ACAGCCAGC TGGTGAAATT GTGCAATTA TACCAATGGA TAAAAAGGT
 CGTGCGGAAA CACCAAAAGA GCTTGCTAAT GTTATATTA TGGCAATGTA TTACGTGACA
 GAAACTAAAT CTAGTAATGG TTTGCTGAAT ATCTTATTA TACCAAAAT CAGTTTAAAA
 TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAATATTA AAGGCAAAAA CCAAGAAATT
 ACTGGGAAA CCACTTTGAC AAAAGAAGAC AAGATATGCT TAATGAGAG TCAAGGAAA
 GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTATATGAA AAGATGCTTA AGCTGTTAAA
 TGGAGTGAAG CTTTAAAAAC AGAATTAGTG AAGGCAATGA AAGCTTTGTA TGAACAGTG
 ACTTTGGCTT TAGATGAAAA GAACCAAGTT GCGCTTATTA AATTAATGAT TAACGAGTAT
 TTCTGGCAAG AAACCAAGC ACCTGAAGGA TATATATTA ATGAAATGGA GTATCCTGTA
 TCCATCAAAA AAGTTGATAA TAACGAAAAA AATTAATTA TACTGAGTA TTTACGGCA
 AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTATTA TACTTATTA GCGCTGATGGC
 ACTGCCGAAA CTGGATTGAA CGACTTATCT TTTAAATGCT TGGATATGA AAGGACCAAN
 GAAATCAGAG GTGCTGAAGA TAAAGCGACC ACATATGTA AATTAATTA AAGTTTGTAT
 GGCTATGGTA AGTTTGAAGA TCTTCCTTAT GGGATATTA TACTTATTA AATAGAGGCT
 CCAGAAGGAT TTCAAAAGAT TACACCACTA GAATATGCT CTACATTTAA GAAAAACAA
 GACGACTATG CGAAGAGTGA GTATGCTTTT AATTAATTA AAGAAATGTA AAAACAACCA
 ATTAAGATGG TGACCTTCC TTACGAGAAA CTAAATTAAC AATTAATTTT TGTAGTCTG
 AACCGTTTGA TGCTTTATGA TTTGCCCGAG AAAGAAATTA GTTATATTA TCTTGCGACT
 TGGAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCAATATAT TGAATAATTG
 AGATATAACT TGCATGAAAT CAAAGAAGAC TGGATATTA TATTAATTA CATTGATGTG
 GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAATATTA AATTAATTA GATTGCCGAA
 ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGATATTA GAAATATTA GCATAAATTA
 ACCGCTGAAC AAGTTTGGGA TAAAGCATC GTCTTATTA ATTATATTA TGAACAACAG
 GTAGCCCTTG AAGCAGGCA TGAGCCAGTA GCGATATTA TATTAATTA CAATCAAGCA
 CAAACCGTCA ATTTGACGAT TGAACGCCAT GTTATATTA AATTAATTA CCACCTAGAA
 GATGGTTGCG AAACCTTTAC TCATGGTGAC GTGATATTA TTTTATTA TGTGCGGTT
 ACCCATGATG TACTGGATGG CTCAAAAGAA GCTTATTA AATTAATTA TGCCTTACTA
 CCAGATGGTA CGAACAAGAA AATTTGAAA TCTGATTA TATTAATTA AGTGAATGAT
 AAAGAATTTA CCAAAACCGT ACTTGCGGAA AATTAATTA CCAAAATTA TCCAGAAGGA
 ACTAAGTTTA CTTTACGGA AATCAATTAC GAAATATTA GAAATATTA TGGAAAACAC
 AATGAAGATT TGAAAGAAA ATCTCAAAAC TTAATATTA AAGAAATTA AACCATACCG
 AGTACGCCAA AACAACCGGA AACACCAGCT GTTCAATTA ATTCTAAGA ATCTAGTCCC
 ACAGTGAAGA CATTCCCGCA AACTGGGGAG AAAAAATTA AATTAATTA GTTAGTTGGC
 TTATCTTGA TTTTTTCGAC TGCTGGGTAT TATTAATTA ATCGCTGCAA TTAA

EF102-2 (SEQ ID NO:394)

MKKTTFKN WSLFATLALL SQTIGGTIGP TIAFADLILH
 PQEVTIHYDV SKLYEVDGTF SDGSTLSERT TSLYALINGA KQTVFOIEPG VSIPTFVTHG
 YQKNPLPMS DKAKLVSVLW EKAGTDIDTN MVAQKMLWEE VNGYKLHSIK RLGGASVDIK
 SIEGKINKAI EEYQKKPSFH NTTVKITLQ STTLINLHNL NLSEFDKVVQ NTANIDYRVI
 GNQLVLTPNS NSKSGTLTLK KSAGTGTPVA YKFAK LTH AGALEKPNFY AIKINVETKG

TABLE 1. Nucleotide and Amino Acid Sequences of the Genes.

```

SLKIKFKDKE  SGDINPETVF  HLEPGKALFF  KIDED  EFL  EILGRIHNT  EWTITEKSVP
DPYMIITTPM  AATIKAGETI  SMTSKNMAIF  SLEED  EFL  EILGRIHNT  EWTITEKSVP
RHDSPAGEIV  QEITTEKGR  AETPKELANA  LELST  EFL  EILGRIHNT  EWTITEKSVP
ANQTVALNVS  NYFGQNQEIT  GETTLLTFEDK  DUNEL  EFL  EILGRIHNT  EWTITEKSVP
SEAFKTELVK  GTHASDETVT  LALDEANQVA  YWDLA  EFL  EILGRIHNT  EWTITEKSVP
IKKVDINNEKN  AVITRDVTAK  EQVIRFGPDE  FHEAG  EFL  EILGRIHNT  EWTITEKSVP
ITGAELKATT  ACNEQLGFDS  YGKFENLPYG  DYLLE  EFL  EILGRIHNT  EWTITEKSVP
DYAKSEYVFT  ITEEGQKQPI  KMTVTPYEKL  TUNEF  EFL  EILGRIHNT  EWTITEKSVP
KDGNNKLNTL  DFTLVKDLR  YNLHEIKEDW  YWVAG  EFL  EILGRIHNT  EWTITEKSVP
TATLANKEKT  GTWKILHKLT  AEQVLLKSIV  LEFNT  EFL  EILGRIHNT  EWTITEKSVP
TVNCTIERHV  SIQTKAHLED  GSQTFTHGDV  MDNFD  EFL  EILGRIHNT  EWTITEKSVP
DGTNKEIWK  GKIEHEVNDK  EFTKTVLAEK  VETBY  EFL  EILGRIHNT  EWTITEKSVP
EDLKEKSQTL  TPKEVPTIFS  TPKQPETPAV  PSAB  EFL  EILGRIHNT  EWTITEKSVP
ILIFSTAGYY  FWNRRN

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EF102-3 (SEQ ID NO:395)

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TT TAGATGAAAA GAACCAAGTT GCGGTTAAAT AC AGCAAT TAACCAAGTAT
TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TATAT TGG ATGAAAGCAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGC TAA TTACTGAGA TCTTACGGCA
AAAGAACAAG TTATTGCTT TGGCTTTGAT TTTT TAA TTGCTGAGC GGTGATGGC
ACTGCCGAAA CTGGATTATA CGATTATCT TTTAA TAA CGGCTTGA AGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGCGACC AAGCTTATA ACGACCAAT AGTTTTGAT
GGCTATGGTA AGTTTGAATA TCTTCTTAT GAGGT ATT TACTTGAGA AATAGAGGCT
CCAGAAAGAT TTCAAAAGAT TACACCACTA GAAAT ATT CTACATTAA GGAACAACA
GACGACTATG CGAAGAGTGA GTATGCTTT ATAT TAA AAGAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTTC TTACGAGAAA CTAATGAGA ACGATTTTC TGTAGTCTG
AACCSTTTGA TGCTTTATGA TTTGCCCGAG AAAGAA ATA GTTTGACTTC TTTTCCGACT
TGSAAAGACG GAAATAAAAA ATTGAATACC CTTTATATA CGAGATAGT TGATAAAATTG
AGATATAAAT TGCAATGAAAT CAAAGAAGAC TTTAT TGG TAGCTCAGC CATTGATGTG
GAAGCTACAA AAGCTGCCCA AGAAAAAGAC GAAAA AGCA AAGCTTGT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ATTGGA CTT GGAAATTTCT CATAAATTA
ACCGCTGAAC AAGTTTGTGA TAAAGCATC TTTT TTTA ATATTTTATA TGAAAAACAAG
GTAGCTTTTG AAGCAGGCAA TGAGCCAGTA TTTAA TATC CTAGCTTGA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTCTTTTC AAACAAAAGC CACCTAGAA
GATGGTTTCG AAACCTTTAC TCATGGTGAC TGAGC TATA TGTTTATGA TGTGTCGGTT
ACCATGATG TACTGATGG CTCAAAAGAA GTTT TAAA CAATTCTTA TGTCTTACTA
CCAGATGGTA CGAACAAAGA AATTGTGAAA TTTGGTAAA TTGACATGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGGCGAA AAGTA TATA CCGGAAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTACCGA AATCAATTAC GAAAA TATG GAAACGTAA TGGAAAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAAAC TTAGC TATA AAGAGTGGC AACCATACCG
AGTACGCCAA AACAACCGGA AACACCAGCT GTTCTTATA ATTCTCAGA AATAGTCC
ACAGTGAAGA

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EF102-4 (SEQ ID NO:396)

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LDEFNQVA VKHLAINEYF WQETKAPEGY TLEETKVF
IKKVDINNEKN AVITRDVTAK EQVIRFGPDE FHEAG EFL AETGFEHISF FUSPLEGTXE
ITGAEDKATT ACNEQLGFDS YGKFENLPYG DYLLE EFL EGFQKITHLE INSTFKENKD
DYAKSEYVFT ITEEGQKQPI KMTVTPYEKL TUNEF EFL RLMLYELIEK EISLTSLATW
KDGNNKLNTL DFTLVKDLR YNLHEIKEDW YWVAG EFL ATKAAQENDE KAKPVVIAET
TATLANKEKT GTWKILHKLT AEQVLLKSIV LEFNT EFL AFRAGNEIVA KASLNNQAQ
TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDNFD EFL HDVLDGSHEA FETILYALLP
DGTNKEIWK GKIEHEVNDK EFTKTVLAEK VETBY EFL KFTFTEINYE HDGNVNGKHN

```


TABLE 1. Nucleotide and Amino Acid Sequence of *E. faecalis* Genes.

EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNQSLSST VK

EF103-1 (SEQ ID NO:397)

TAAGATAGGT TTATCAAAGA AAAGGAGCGA TGGTTLTGA AAAAGAAAGT ATTAAGTTGG
 ATTACTTTAG TAACATTAAG TACGTTACTT ATNGGCTTT ATGCAAGTCC AGCATTGCA
 GATCATGCAG CCAATCCAAA TAGTGCTACA GCAAAATTAG GCAAACATCA AAACAATGGC
 CAAACAAGAG GCGACAAGGC GACTAAGATT TTATTTTGA CCGACTGGCA AGGAACCCGT
 GTTTATGATG CTGCTGGTAA TGATTTAAGC GAGAAATATG CTAATTTTAT TGGTTTAGCA
 AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCAGA AAAATACTGG GGAACCCGT
 GGTGACGAAG GAACATTTTT TGTGACAGGT GATGCTTCAA AACGAATTTT AATTTCGCGG
 ACACAAAATT ATCAAGCCGT AGTGGATTTA ACGGATTTGA GTAAAGACNA ATTTACTTAC
 AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGCTTCAA TTTACGTGCA ACACATCCCT
 TATCATGGGA AAAAATTAGC TTTTACAAAT GAGCTTGAAG CATTAACTAA TCAAACTGGC
 AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTTCAGA CAACCTTTTG GAATGGCACA
 AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCTTGA ATCAAAATTT CATTAGTTTA
 GCGAAATTTG ATCCAAACAC AAGTAAATAT GATTTTCTTA ATTTACAAAC AGGTGAAACC
 CGCGGCGACT TTGGGTACTT CCAAGTGGTG GAGAAATACA AGATTGGGCG CCATGTATCT
 ATTGGTACGA ATCGTTACGG CGCGGCGCTA GATTTTGAAG AACTAAACAA TGATCGATTT
 ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATATA TTCAAGTETT CGTGGAACAT
 GAACCTTACC AAGGCACATA TCATCCAGCC TTTATCTTCT AA

EF103-2 (SEQ ID NO:398)

MKKKVLSSI TLVTLSTLLI AGYASPAFAD HAANPNSATA NLGKHQNNQ
 TRGDKATKIL SGTDWQGTRV YDAAGNDLTA ENANF LAK YDGETSFTEF FDKNTGETRG
 DEGTFFVTGD GTRKILISRT QNYQAVVDLT EVKNTTCTK RLKDKKLAND VEYVVEHIPY
 HGKKLAFTNG REALTNQTGK IVTNKSGDKI LSTT LCTK YVDKNSNEVT AANQNFIsla
 KFDPNISKYE FPNLQTGETR GDFGYFQVVD NKKIRADYI STNRYGAALD LTELNNDRFT
 YTRMGKDNAG NDIQVFVEHE PYQGYTHPAF TF

EF103-3 (SEQ ID NO:399)

TCATGCAG CCAATCCAAA TAGTGCTACA GCAAAATTAG GCAAACATCA AAACAATGGC
 CAAACAAGAG GCGACAAGGC GACTAAGATT TTATTTTGA CCGACTGGCA AGGAACCCGT
 GTTTATGATG CTGCTGGTAA TGATTTAAGC GAGAAATATG CTAATTTTAT TGGTTTAGCA
 AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCAGA AAAATACTGG GGAACCCGT
 GGTGACGAAG GAACATTTTT TGTGACAGGT GATGCTTCAA AACGAATTTT AATTTCGCGG
 ACACAAAATT ATCAAGCCGT AGTGGATTTA ACGGATTTGA GTAAAGACNA ATTTACTTAC
 AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGCTTCAA TTTACGTGCA ACACATCCCT
 TATCATGGGA AAAAATTAGC TTTTACAAAT GAGCTTGAAG CATTAACTAA TCAAACTGGC
 AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTTCAGA CAACCTTTTG GAATGGCACA
 AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCTTGA ATCAAAATTT CATTAGTTTA
 GCGAAATTTG ATCCAAACAC AAGTAAATAT GATTTTCTTA ATTTACAAAC AGGTGAAACC
 CGCGGCGACT TTGGGTACTT CCAAGTGGTG GAGAAATACA AGATTGGGCG CCATGTATCT
 ATTGGTACGA ATCGTTACGG CGCGGCGCTA GATTTTGAAG AACTAAACAA TGATCGATTT
 ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATATA TTCAAGTETT CGTGGAACAT
 GAACCTTACC AAGGCACATA TCATCCAGCC T

EF103-4 (SEQ ID NO:400)

HAANPNSATA NLGKHQNNQ
 TRGDKATKIL SGTDWQGTRV YDAAGNDLTA ENANF LAK YDGETSFTEF FDKNTGETRG
 DEGTFFVTGD GTRKILISRT QNYQAVVDLT EVKNTTCTK RLKDKKLAND VEYVVEHIPY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. coli* Genes.

RGHKLAFSTNG REALTNQTGH IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI IUTNHSSEFI
 KFDPNSTKYE PFNLQTGETR GDFGYFYWE DDFYFYWE DDFYFYWE DDFYFYWE DDFYFYWE DDFYFYWE
 YTRMGKDNAG NDIQVFWEHE PYQSTVHIA

EP104-1 (SEQ ID NO:401)

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 GCACAAAATT TCGGGTTTTC TGTAAATGTC TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GAGACCACTG ATACAGCAAA AAAAGAGGGA GATTTCGGA ACTCAACACC ATCTTTTACCT
 TTAGCAACAA CGACTACTTC AGAAATGANT GAAAT ACTG CAACAACTGA ATCGCAAAACC
 ACAGAGGCGA GCACAAACAT TTCCAGTATC CTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GAGGACAAAG ACACCTCACT TAATGAAAAA GATT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 BATGAACATC TTGACAGTAT GATTTTTCG GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GAGTTTCACC GCGAATTAAA TACAACAGCG GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AACACAGGTT ATGCACTTTC ATGATTTTAT AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 TCAACTTCTA GCGGAGAAAT GACAGGATTT GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AAAACATTAA GTATTACGTT TAATCAATTA TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AAAAGTTATC TAACAACABA GCGGGAATTA TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AAAAAAACCT ACTCGTTTGA TTTATATGAA CAATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ACCAGAACGA CCGGTTTAGA TGCGAAATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AATCAAAACAT TAGAATTATT AACAACAGAG ACTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AACCTTGAAC CTCAGGTTTT CATTATGAT GTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ACGCAAAACCT TGTAAACACC TGGCAAAAT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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 ACAATTTATT TAGAGAGTGC TCGGAGTAT AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ACAAAAATTG GGTCAATTTT TTTGAAAAT AGCAAGGAA CTAAACAAAC AATCGATTTT
 ACTGCTAAGA CGAGTCAAAAT AATGAAATTA ATTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 TATATCAGTT TTCAAAGCAA AGCGAAATAT TATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ACAAAGTGG GTCAACAAAT CGTATTAAG ATTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AAAATTTACG CGTATGCTTC TTTATATGAA AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AAAACTGAAG GTGGCAAGCT CACTTTAAAT GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ATTTCTGATT TAACAATGGA TTTTGACAAAG AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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 GTTGTAAATC CTTTGAATGC TGAAACTTCT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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 ATTAAGGTAA AGCATCCTAA TTATCTTTCA TTACGAGCTA CAAAAGAAAT TTATTTTAT
 TACAAGTTAG GAACGGATTA TACAGTAACG CCAAGCTCAG ATGGTTTCACT TATTAAGTTC
 ACTACGCCAA TAACCAACGA AATCCAAAT CCAATTTGTT TTAATTATGT GCGAGATAGT
 TTGCCAAAAG ATAAAAGTAT CCCAGTCTAT AGGATTCGA TAACAATGAG TCGTGAAGGT
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 CAAAGTAGTA AAAATCAATT CCTTTTCAAT GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GTCCGTACAA AATTTCCAGC TGGCGCTBAT GTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GATCAGGTAG ATTCAATTTA TCCACAATAC TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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 TGGATCGACG TGCCAACCTCT TTATATAACA GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AATGAAGGCT CTGCTTCGGT TTCTGTTCAA AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 CAAGCGGCGA ATCCAACATT AAAAAATTTA AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 GATAATAAAA CACATCGTGT GAAAAATCCA AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 AATGCTCAAA TCGATTTGAA TTCTATTACC GTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 TTAGAGAAGA CTACAAACGG TGCGAAAGTC AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ATTACGATTG AATACAATAC GGTCTCTTCA AATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ATCGACTCTG AAACATTGAA CCAGATGTCT GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 ATCACATTGA AATTTCTAGA AGGTGATTCG GATTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTCTACACGC ATAACGTAGA GGATGAAAAC CAGGCGATTG CGAAGGTTTC TTTTGAAC TA
 ATTGATAATG TCACGCATAC AGCAACCGAA TTAAACACAG ATGAAAAGG TCAATACTCC
 TTTGATGCCA TCATGACAGG TGATTATACT TTGCGGTAA CGAATGTACC GCAGGAATAT
 TCCGTGGATG AAGAGTATTT GACAGGAAAA GGCATTAAAGC TGGTCAAAAG AGACAACCAA
 CTAAAAATTC CATTAAACGAA AACAATTGAT CACAGTCGTT TACAAGTCAA AGATTCAACG
 ATTTATGTCG GCGATTCATG GAAACCAAGAA GAGAACTTTG TTTCAGCAAC AGATAAAACA
 GGTCAGACG TTCCCTTCGA AAAAATCACT GTTTAGGTC AAGTTGATAA CANCAAAGCA
 GGCCTTTATC CAATTATTTA CAGTGACGAA GGTAAAGAAG AAACAGCCTA TGTGACCGTC
 AAACCCGACC AATCTAAGTT AGAGGTCAAA GATAAACGA TTTATGTTGG TGATTTCGTGG
 AAACCAGAAG ATAATTTTCGT TTCAGCGACA GATAAACAG GTCAAGAGCT NCCGTTTGAA
 AAAATTGATG TTCAGGGAAC AGTGAATGTT GATTAATAG GCGATTATGA AATTGCTCTAT
 AAAAATGGCA NAAAAGAAGC GAAAGCAATC GTTCCTGTC GTGATGACAG TCAGTTAGAG
 GTTAAAGATA CAACGATTTA TGTGGTGTAT TCGTAAAC CAGAAGATAA TTTCGTTTCA
 GCAACAGACA AAACAGGCCA AGACGTTCCG TTGAAAAA TCACTGTTTC AGGTCAAGTT
 GATACTAGCA AAGCAGGCGT TTATCCAATC GTTACAGTT ACGAAGGTAA AGAAGAAACA
 GCTAATGTGA CTGTCAAACC CGACCAATCT AAGTTAGAGG TTAAAGATAC AACGATTTAT
 GTGGGCGATA AATGGGAACC AGAAGATAAT TTCTTTTCAG CAACAGACAA AACAGGTCAA
 GATGTCCCGT TTGAAAAAAT TGACGTTTCAG GGAAGAGTGA ATGTTGATAA AATAGGCGAT
 TATGAAATTG TCTATAAAAA TGGCACAAAA GAGGCAAAAG CAATCGTTCA TGTCCGTGAT
 GACAGTCAGT TAGAGGTCAA AGATACAACA ATTATGTCG GTGATAAATG GSAAGCAGAA
 GATAACTTCG TTTCCGCGAC AGACAAAACA GGTAAAGACG TTCCGTTTGA AAAAATTGAT
 GTTCAGGGAA CAGTGAATGT TGATAAAATA GGTGATATG AAATTGTTTA TAAAAATGGC
 ACAAAGAAG CGAAAGCAAT CGTTTCATGT GGTGATGATA GTCGTTTACA AGTCAAGGAT
 ACAACGATTT ATGTCGCGCA TTCNTGSANA CCAAAENGA ACTTGTTTC AGCNACAGAT
 AAAACAGGTC AAGATGTCCC ATTCGAAAAA ATCACTGTT

EF104-2 (SEQ ID NO:402)

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 ATTTTSEMNQ PIATTESQTT EASTTASSDA ATPSEQTTE DKDTSLNEKA LPDVQAPITD
 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATEQFAVGN TGYAPGSVYT VQLPEHLGYS
 TVSGEVTGIG ATWAVDAATK TLSITFNQRV SETSEFVELK SYLTTEAEPL IKIETPGKNK
 KTYSFDLYEQ VEPIQYNERT RTTGLDGEIF YRLDRLTGNN QTLELLTTET PGAVFGKQDN
 LEPQVFSYDV DINGQILPET QTLTTPGKDY TNSDNLGRI AVTVPNMNMQ KAYSLSINRT
 IYLESASDYN YLYSQQYPTT KIGSISLKST TCTHQTDFD AKTSQTSKVI ADREMRMSY
 ISFQSKGKYY VTLYGTLTET KVGQQIVLES TGGQENKNPK FTAYRPLVEN VFLEDYFDIK
 TEGGKLTLLTA TKDSYLRLNI SDLTMDFDKK TINKSLTPV IGPNEAQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KEFPTANLEI KVKHPNYL SL FATKEIYFYY
 KLGTDYTVTP TSDGSVIKFT TPITNEIQIP IGFNYPDSL PKDKSIPNDT IPITMSAEGL
 TPVDITVTTN SKRGSERTLQ SSKNQFLVNA ENLSFISLSV RTKIPAGREV LFDIYDVSND
 QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TPDENTINSYT FDFGKTNRY IIEYKNANGW
 IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALDILSATQ AANFTLKINT KTTVTTKNID
 NKTHRVKNPT IELTPKGTIN AQIDLNSITV KGVPELAYSL EKTINGAFVI FHDYTLTENI
 TIEYNTVSAN AGQIYTETTI DSETLNQMSA SKKKVTAPI TLKFSEGIKAE GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVHTTATEF TDEKQYSF DAINTGDTL FVTNVPQEYS
 VDEEYLTGKA IKLVKGDNL KIPLTKTIDH SRLQVNDSTI YVGLSWKHEE NFVSATDKTG
 QDVPFEKITV SGQVDNXXKAG VYPIIYSDG KBEATAVTVK PDQSKLETKD TTIYVGDSWK
 PEDNFVSATD KTGQDVPFEK IDVQGTVMVD KIDYHIVYK NGXKEAKAIV HVRDSSQLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVPF EHLTVSQQVD TSKAGVYIV YSYEGKEETA
 NVTVPKPDQSK LEVKDTTIYV GDKWEPEDNF VBATDKTGQD VPFEKIDVQG TVNVDKIGDY
 EIVYKNGTKE AKAIHVHRDD SQLEVKDTTI YNGDAWEAED NFVSATDTG QDVPFEKIDV
 QGTNVNDKIG DYEIVYKNGT KEAKAIVHVR DLSRLQVKDT TIYVGDSWXP EXNFVSATDK
 TGQDVPFEKI TV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

EF104-3 (SEQ ID NO:403)

TGTAA CAACGACAGA AGGACAAACA
 GAGATCACTG ATACAGCAAA AAAAGAGGCA CATTATCGA ACTCAACACC ATTTTACCT
 TTAGTAACAA CGACTACTTC AGAATGATC TAACTACTG CAACACTGA ATGGCAACC
 ACAGAGGCGA GACAAATGAC TTCTAGTATC TAACTACAC CATCTGATTA ACAAACAACG
 GAGSACAAGG AACCTTCACT TAATCAAAAA GTTTTGGCAG ATGTTCAACC GCGAATTACA
 GATGAACATC TTGACAGTAT GAGTCTTTTCG CCAATGCTG GAACAGATTA TACCAAAACA
 GAGGTTTACC GCGAATTAAA TACAACATCG GTAAACGATA CGTTCCCAAT TGTGTTGGGA
 AACACAGGTT ATGCACTTGG ATCACTTTAT ACAGTTCAT TACCAGAA CA TTTAGGTTAT
 TCAACTGTCA GCGGAGAAAT GACAGGCAAT GCTTAAATTT GGGCAGTCCA TGTGCGGACC
 AAAACATTAA GTATTACGTT TAATCAAGCA GTTTAGATA CTTCCTTTAA AGTAGAATA
 AAAAGTTATC TAAACACAGA GCGGAAACGA TTAACCAAAA TTGAACACTC AGGAAAAAAT
 AAAAAAACCT ACTCTTTTGA TTTATATGAA TAAGTGGAAC CAATTCAACA TAACGAACGA
 ACCAGAACGA GCGGTTTAGA TGGTGAACAT TTTTATAATT TAGACGGAAT GTTAACCTGGC
 AATCAACAT TABAATTATT AACAACAGAG AATTAAGCG CTGTCTTTGG AAAACAAGAT
 AACTTGGAAC TCAAASTTTT CATTACGAT TTGACATTA ATGCTCAAT TTTACAGAA
 ACCTCAACCT TTTTAAACAC TGGTAAAGAT TATAATTAA GCGATAACTC ACTGGGCGCG
 ATTCTGTAA CTGTTCCAAA CATGAATCAA TAAAAAGCT ATTCCTTATC GATTAAATCGG
 ACAATTTATT TAGAGASTGC TTGGGACTAT AACTACTTAT ATTCGACCA STATCCAACA
 ACAAAAATTG GGTCAATTTT TTTGAAAAT AGGACAGGAA CTAAACAAAC AATCGATTTT
 ACTGCTAAGA CGAGTCAAA AATAAAATA ATGCTGATC TGAATGCTG TAGATGTCC
 TATATCAGTT TTCAAAACAA AGGGAATAT TATTAACAA TTTATGGAC GTTAACAGAA
 ACAAAAGTGG GTCAACAAAT CGTATTAGAG ACTACAAACG GTCAAGAAAT TAAGAAATCCT
 AAATTTACGG CGTATGCTC TTTATATGAA AATTTAAAA TGGAAAGACTA TTTTGATATT
 AAAACTGAAG GTGGCAAGCT CACTTTAAG AGGAAAAAG ATAGCTATTT AAGAAATAAT
 ATTTCTGATT TAACAATGGA TTTTGACAA AAGGACATTA ATCTATCAT AATACACCT
 GTAATTGGTC CTAATAAAGC CATTCAATTA AATTCGATC AATATATGA ACCAATTAGT
 GTTGTAAATC CTTTGAATGC TGAAACTGCT TGGTAAAT ATGATCAAAA TGTCTCCTAT
 TCATCAAGAA CAACGTGCTC AGTTATGGA AGCAAGAGA AACCAGTCA AATTTAGAA
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 TACAAGTTAG GAACGGATTA TACAGTAAAG CCAAGTCAAG ATGGTTCAAT TATTAAGTTC
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 TTGCCAAAAG ATAAAAGTAT CCCAGTGGAT AGGATACCGA TAACAATGAG TGTGAAAGT
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 CAAAGTAGTA AAAATCAATT CCTTGTCAT GCAGCAAAATG ATTCCTTTGA CTCACTAAGC
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 GATCAGGTAG ATTCAATTTA TCCACAATAC TGGGACCGCG GTCAATACAT TCAATAACCA
 ATGACGCCAA ACAGCCCTGG ATATCCAAG ATTACTTTTG ACGAAAATAC CAATAGTTAC
 ACGTTTGATT TTGGAAAAAC CAACAAAGCT TAAATATTG AGTATAAATA CBTCAATGGC
 TGGATCGACG TGCCAACTCT TTATATAADA GCGATAGCGA AAGAACCAAA ATCGAATAAT
 AATGAAGGCT CTGCTTCGGT TTCTGTTCAA AATTAAGCGT TAGACATTTT GASTGCAACA
 CAAGCGGCGA ATCCAACATT AAAAAATGTA AATTAACGA CAGTACAAAT AAAAAATATT
 GATAATAAAA CACATCGGT GAAAAATGCA ACATTTGAAT TAACACCAAA AAGCAACACC
 AATGCTCAAA TCGATTTGAA TTCTATTACG GTGAAGGCG TGCCAGAGA TGTATTTC
 TTAGAGAAGA CTACAAACGG TGGGAAAGTC ATTTTAAAG ACTATACAT TACAGAAAAC
 ATTACGATTG AATACAATAC GGTCTCTGCA AACCTTGGCC AATCTATAC AGAAACAACA
 ATCGACTCTG AAACATTGAA CCAGATGCTT GGTATCAAGA AAAAGTCAAT CACTGCGCCA
 ATCACATTGA AATTCTCAGA AGGTGATGCG GAAGCTATTG TTTATTTAGC AACTGCCACA
 TTCTACACGC ATAACGTAGA GGATGAAAA CAGCAATTTG CGAAGSTTTT TTTTGAACATA
 ATTGATAATG TCACGCATAC AGCAACCGAA TTTTAAACAG ATGAAAAAG TCAATACTCC
 TTTGATGCCA TCATGACAGG TGATTATACT TTGAGAGTAA CGAATGTATC GCAGGAATAT
 TCCGTGGATG AAGAGTATT GACAGGAAAA GCAATTAAGC TGGTCAAGGG AGACAACCAA
 CTAAAAATTC CATTAAACGA AACAAATGAT CACTCTGTT TACAAGTCAA AGATTCAACG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATTTATGTCG GCGATTCATG GAAACCAGAA GABAA TTTG TTTCAACAAO AGATAAAACA
 GGTCAGACG TTCCCTTCGA AAAAATCACT GTTTCAGSTC AAGTTBATAA CAIICAAAGCA
 GGCGTTTATC CAATTATTTA CAGTGACGAA GGTAA GAAG AAACAACCTA TGTGACCGTC
 AAACCCGACC AATCTAAGTT AGAGGTCASA GATAACABBA TTTATBTTEB TBATTEGTGG
 AAACCCAGAAG ATAATTTTCGT TTCAGCGACA GACAA ACAG GTCAAGACAT NDCGTTTGAA
 AAAATTGATG TTCAGGGAAC AGTGAATGTT GATAAAATAG GCGATTATTA AATTGTCTAT
 AAAAATGGCA NAAAAGAAGC GAAAGCAATC GTTCAAGTCC GTGATBACAG TCAGTTAGAG
 GTTAAAGATA CAACGATTTA TGTTCGTGAT TCBTB AAAAC CAGAAATATA TTTTCGTTTCA
 GCAACAGACA AAACAGGCCA AGACGTTCCB TTTCA AAAA TCACTBTTCB AGBTCAAGTT
 GATACTAGCA AAGCAGGCGT TTATCCAAATC GTTAAAGTT ACGAABGTAA AGAAGAAACA
 GCTAATGTGA CTGTCAAACC CGACCAATCT AASTTAGAGB TTAABATATC AACGATTTAT
 GTGGGCGATA AATGGGAACC ACAAGATAAT TTBSTTTCAG CAACABACAA AACAGGTCAA
 GATGTCCCGT TTGAAAAAAT TGACGTTTCA GBAACAGTBA ATGTTBATAA AATAGGCCAT
 TATGAAATTG TCTATAAAAA TGGCACAAAA GAABCGAAAG CAATCBTTBA TGTCCGTGAT
 GACAGTCAGT TAGAGGTCAA AGATACAACA ATTTATGTGG GTGATAAAG GGAAGCAGAA
 GATAACTTCG TTTCCGCGAC AGACAAAACA GGTCAAGACG TTCCGTTTBA AAAAATTGAT
 GTTCAGGGAA CAGTGAATGT TGATAAAATA GGBATTATG AAATTBTCTA TAAAAATGGC
 ACAAAAGAAG CGAAAGCAAT CGTTCATGTC CBTBATGATA GTCGTBTATA AGTCAAGGAT
 ACAACGATTT ATGTCGGCGA TTCNTGGANA CCABAAGNGA ACTTTBTTCB AGDNACAGAT
 AAAACAGGTC AAGATGTCCC ATTC

EF104-4 (SEQ ID NO:404)

VTTTEAQTE TTDATKEAE LSNSTPLPL
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 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATTCFAVGN TGYAFGSVIT VQLPEHLGYS
 TVSGEVTGIG ATWAVDAATK TLSITFNCFV SIISFKVELK SYLTTEAEEL IKIETPGKNK
 KTYSFDLYEQ VEPIQYNERT RTTGLDGEIF YNLEETLTGN QTLELLTET PGAVFGQDN
 LEPQVFSYDV DINGQILPET QTLTTFGKPY TLSENLGRI AVTVPIIMNQ KAYSLSINRT
 IYLESASDYN YLYSQQYPTT KIGSISLKST TGTCTTDFE AKTSQTSKFI ADEMRMSY
 ISFQSKGKYY VTIIYGLTET KVGCCIVLES TNGQBIKNPK FTAYGPLYEN VKLEDYFDIK
 TEGGKLTITA TKDSYLRINI SDLTMDFEKK DNLNLSSTPV IGPNEAIQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KENFIQNLFI KVKHPIYLL FATKEIYFY
 KLGTDTYVTP TSDGSGIKFT TPITNEIQIP IGFNYVFDL PKDKSIPVT IFITMSAEG
 TPVDTTVTN SKRGSERTLO SSKNCFIATA FMSFDSLSV RTKIPAGADV LFDIYDVSND
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 NKTHRVKNPT IELTPKGTN AQIDLNSITV KGVFEDAYSL EKTNGAPVI PKDYTLTENI
 TIEYNTVSAN AGQIYTETI DSETLNQMSA SHKVTAPI TLKPSGDAB GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVHTATFP TTBEGQYSF DAIMTSDYTL FVTNVPQEYS
 VDEEYLTKGA IKLVKGDNL KIPLTKTIDH SLLQVKDSTI YVGDSWKPEE NFVSATDKTG
 QDVPFEKITV SGQVDNXXAG VYPIIYSDG KEETAYVTVK PDQSKLEVHD TTIYVGDSWK
 PEDNFVSATD KTGQDVPFEK IDVQGTNVND KIGDYEIVYK NGXKEAKAV HVRDDSQLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVPF EKITVSGQVD TSKACVYPTV YSNEGKEETA
 NVTVKPDQSK LEVKDTTIYV GDKWEPEDNF VBATDKTGQD VPFEKIDVGB TVINVDKIGDY
 EIVYKNGTKE AKAIHVHRRD SQLEVKDTTI YVSDPWEAED NFVSATDKTB QVVPFEKIDV
 QGTNVNDKIG DYEIVYKNGT KEAKAIHVHR DSRLOVHDT TIYVGDSWKP EXNFVSATDK
 TGQDVPF

EF105-1 (SEQ ID NO:405)

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 GTTCCTGCTG AAGCGGCGAC GGTCGTTTTT GATAGCGAAC AGTCGATTTT TTTTACCCCA
 AGCACAGATG GGACGGATCC AGTAAATCA GAAAATCCCG ATCCAGAAAA ACCAGTTTCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGTCGATC CAACGAATCC TGAAGAACT AATCGAGGTA CCCCTGATCC AGTTTCCATC
 GATTATGCCT CAAGTTTGGT TTTTGGGAGT AATGAGATAT CGAATAAGSA TCAAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGGTGAG CAAGTGAAAT GGTAACTGCT
 AATTATGTAC AAGTAAGTGA TTTAAGGAGA ACCAATGCTG GCTGGGTTT AAAAAGTGAAA
 CAAAATGCTC AATTTCTGTA TGCAGAAACA TTACACAAAG AATTAAAGG CGCCACCGTC
 GCCTTTACTG AGCCCGAGT TGGTCAAAAT GCGAGCGAGT TATTGCAGC AATTGCTACC
 GCAAACATTC AATTAGATGC TGGGGGGGCA GAAAGTGTG TCATGCAAGC CCGAGAAAAG
 ACCGGCGGCC GAACGTGGAT CAGGTGTGCG GGGCAAGCAG AAAAAGTGAC CCAAAAAAAT
 CAACAAGGAC AGCAAGTAAA TGCACAAATC ACACGGGCAA TCTCACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAAT ACAATTTAAA ACAACATTC CTTGGCTACT TTAAATGTGA
 CCAGTAAATA ATGGAGGGAA ATAA

EF105-2 (SEQ ID NO:406)

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 VDPTNPDPGN PGTPGPLSID YASLDFGSN EISNKDQTYF ARAQTYRNPD GSASELATAN
 YVQVSDLRGT NAGWVLKVQ NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVNAIT IT RAISLTVPGK
 TPKDAVQYKT TLTWLLSDVP VNNGSH

EF105-3 (SEQ ID NO:407)

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 AGCACAGATG GGACGGATCC AGTAAATCCA GAAATCCCG ATCCAGAAAA AGCAATTCGA
 CCAGTCGATC CAACGAATCC TGATGGAGCT AATCGAGGTA CCCCTGATCC AGTTTCCATC
 GATTATGCCT CAAGTTTGGT TTTTGGGAGT AATGAGATAT CGAATAAGSA TCAAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGGTGAG CAAGTGAAAT GGTAACTGCT
 AATTATGTAC AAGTAAGTGA TTTAAGGGGA ACCAATGCTG GCTGGGTTT AAAAAGTGAAA
 CAAAATGCTC AATTTCTGTA TGCAGAAACA TTACACAAAG AATTAAAGG CGCCACCGTC
 GCCTTTACTG AGCCCGAGT TGGTCAAAAT GCGAGCGAGT TATTGCAGC AATTGCTACC
 GCAAACATTC AATTAGATGC TGGGGGGGCA GAAAGTGTG TCATGCAAGC CCGAGAAAAG
 ACCGGCGGCC GAACGTGGAT CAGGTGTGCG GGGCAAGCAG AAAAAGTGAC CCAAAAAAAT
 CAACAAGGAC AGCAAGTAAA TGCACAAATC ACACGGGCAA TCTCACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAAT AC

EF105-4 (SEQ ID NO:408)

ATVVFVFD SEQSVFTPS TDGTDVNPPE NPDPEKPVVP
 VDPTNPDPGN PGTPGPLSID YASLDFGSN EISNKDQTYF ARAQTYRNPD GSASELATAN
 YVQVSDLRGT NAGWVLKVQ NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVNAIT IT RAISLTVPGK
 TPKDAV

EF106-1 (SEQ ID NO:409)

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 AATCCCAATA ATTTAGGGGA TTTAAGTGAG TATTTACGTT CAGTTGCTAT TAGADAAGAT
 GAAGGATTAT CAGAAAAAGA TTGGGCTGGA ACACGCGTTT ATGATCGAAA TGGGAATGAC
 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAAT TTGATGCAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACTGAGAAA TCAACAGGAG ATGAAGAAC CTTCTTTATG
 ACCGCTGGTA TTACAGATGT TTCCCGTCTT GTAATTATTT CTGAAACCAA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTC GTAGAAAAACA AAGCAACCTC AGGACAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TATGGTCGTC CGCAGCCATA CCCCATAAT CGTCCCAGAA CACTAGAATT CACGAATGGA
 CGCCGTGCCA TGACAGAACA AACAGGCCAG ATTGATGTAA ATCGACAAGG GGATGAAATT
 ATTGGTAAAA CTTCTTTTGA TGGGACACCG CAACTTCTTT GGAATGGGAC AAAAGTAGTG
 GATAAAGATG GCAATGACGT AACTTCGCCC AACCAAACT TTATCAGCTT AGCGAAATTT
 GACCAAGATA GCAGCAAATA TGAATTTTTC AATTTACAAA CTGGTGAAC TCCTGGCGAC
 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCGTG CCCATGTTTC CATTGGAACC
 AATCGCTATG GCGCTGTCTT AGAGTTAACA GAATTGAATG ATAATCGTTT TACGTACACA
 CGAATGGGTA AAGATAACGA AGGAAACGAT ATCCAAGTCT ATGTGGAACA TGAACCATAC
 CAAGGAACCT TTAATCTGA ATTTACCTTT TAA

EF106-2 (SEQ ID NO:410)

MKKKIVGT ITLLALSALL VGGAGGALTA EAYVPQSVN PNNLGLPEY LRSVGIRQDE
 GLSEKDWAGT RVYDRNGNDL TDENQNLHA IKFDATTSFY EFPDKETGES TGDEGTFMT
 AGITDVSRV IISSETKNYQG VYPLRTLYQD TFTYRQMGKD KNGNDIEFV ENKATSGPVY
 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGDIEI GKTSFDGTPQ LLWNGTKVVD
 KDGNDVTSAN QNFISLAKFD QDSSKYEFPN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAVLELTE LNDNRFTYTR MGKDNENNDI QVYVEHEPYQ GTFNPEFTF

EF106-3 (SEQ ID NO:411)

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 GAAGGATTAT CAGAAAAAGA TTGGGCTEGA ACACGCGTTT ATGATGAAA TGGGAATGAC
 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAT TTGATGAAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACTGAGAAA TCAACAGGAG ATGAAGGAAAC CTTCTTTATG
 ACCGCTGGTA TTACAGATGT TTCCCGTCTT GTAATTATTT CTGAAACCAA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTC GTAGAAAACA AAGCAACCTC AGGACCAGTT
 TATGGTCGTC CGCAGCCATA CCCCATAAT CGTCCCAGAA CACTAGAATT CACGAATGGA
 CGCCGTGCCA TGACAGAACA AACAGGCCAG ATTGATGTAA ATCGACAAGG GGATGAAATT
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 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCGTG CCCATGTTTC CATTGGAACC
 AATCGCTATG GCGCTGTCTT AGAGTTAACA GAATTGAATG ATAATCGTTT TACGTACACA
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EF106-4 (SEQ ID NO:412)

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 GLSEKDWAGT RVYDRNGNDL TDENQNLHA IKFDATTSFY EFPDKETGES TGDEGTFMT
 AGITDVSRV IISSETKNYQG VYPLRTLYQD TFTYRQMGKD KNGNDIEFV ENKATSGPVY
 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGDIEI GKTSFDGTPQ LLWNGTKVVD
 KDGNDVTSAN QNFISLAKFD QDSSKYEFPN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAVLELTE LNDNRFTYTR MGKDNENNDI QVYVEHEPYQ GT

EF107-1 (SEQ ID NO:413)

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 ATANATANAA AAATGCTAGT TATCAGTATC GATAATAACA GGATACTCAT TAAGAAAGGA
 CTTTATAGAG ACTATAGATT GAATTTTAC ATAGAAAGAA GGAGCAAGAT GAAGCGAGTA
 AATTGAAAA GATGGCTAGT TGTGGGTTA AGTTGTTCTT TGTTCATGGA TTCAGTGGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGTGTGACTG TGTTAGGGBA AAGGATTACT GGGGGGAGCA AGCAAGGAMI ASCAACATCT
CAGTCGAGTS ACGAABGBAB CCABAGBACB CAACACACCB AAGAGTCABA GGCACCGGTC
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TTGTTTGATC CCGACCGAAT TACBAGBGB BTCAATCTTT CCACGTTTTG OTTTTATGAA
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ATTCGCAACGT CACGAGTTT TAAATATGAT ACAAATAACB AGAATCCAGB TAATATTTAT
GGCGTTTTCTG AAGTGTGGTT TACTATGCT AAGBAGPATB AAGGCTGBA GATTBACCA
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GGGGGCAAG TGAAGAACTA TGTGGGBGB AATBGBABA CGGAATTAGA GTTAAACCAAT
BAAAAAATGC CCAATAAGCT BACSTTGBT CCAAAAAABA CGTTTAAATA TACBGTAGCT
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CGTGTACCGG AAAAAATTBA GAATCCGBA GCGGGGGBA TTCCTGGBB AGAABSTTAT
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TTGCTTGAAC GTTACACAGB BGTGATGBB AAGACGTATT TATTTAABGB TBTBTACAAA
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GATGACAATG ACGATTTCBA TGTGCTTAT GAAGAAGCAB TGATGAAAC BTATACGTTG
CCAGCGAGAG AAGCTTTGTT CCGCTATGTT GATGAGCAAB GAAACTTCAT TAATCCCGCC
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CAAAAAGTCT ACACACGCB AGACBAGGB ACAATGBTA CTATGGBCB GBAAGATG
AGTGTGAAA TTCCTAAGTA TTACBAGACG ATTTGATTT CACCAACTAB TGBTATACA
GGGGATAAAA CCAAGTATCC AGTACCAAT GAAGTGBGB GTGGCATBA AAACCCGAC
AACATTGTTA GTAGTTTAST GGBAANCNT GCGTATAACT TGACCCAAA AASTGCCACA
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ACGGCCGCTG CTGCCAGCTT TACCGATTAC AACCAACCAA CAGAAACBAG GACACCACTT
GGCAAGACCA GCACCGTGAC TTTAACCGCC GACAATACB CAACAGCBT GGTGCAAAC
CAACAGTTCA CAGGCAGTGA CGTCTATCAG TTGGACTTBA CGTTTGCTAA CATCAACTA
GAAGTGCCAG CCAACCAAGG TATGGCTGGC CAACAATACT AAGCCGCBT CACGTGGAAT
TTAGTGACTG GCCCCTAA

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EF107-2 (SEQ ID NO:414)

MKRVN

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SEAKTVPPQE TARIASRAIG YSSVEGREIP FFFVEEDGTL FDPDRITMAN NLSTFSFYEE

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KLQRTPLEPT	TVNNGKLLSI	PTSPAFKYDT	NNQNPSNIYG	VSEVSFTTPK	EYQSLDIRPS
TFYTGDDTQY	PVPTVFANVG	GKVTNYVGAN	AETELELTNE	KMPNKLTFBF	KKTFKYTVAT
APGGVITYALT	YFYGDVGGPT	SSHQRRGTAG	PVYYLTKHR	VTEKFENFAC	GAIPAPEGYT
QDKKTIIVTGE	DFTFTQEGTL	PERYTGSDGK	TYLFKGWYFG	NAKPSTLEPT	KTPSYAVTYD
DNDDLHVVE	EAVMKTITLP	AREALFGYVD	EQCNLINPAK	FKLSATHSES	DGATGEMTTF
PTIDGIDMPA	SQKKKLAIPQ	KVYTRPDDGT	IVTYGPQEV	VEIPKYVQTI	SISPTTAYTG
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IYSGTAGGNY	NLSTPDGTIY	YYLENRRVTE	HFVDESGAHI	TPPTGFTQBN	QLVVDSENVY
YTVAKALPKI	YQAGEKTYIF	CGWFKGKTKP	ATLKTTTTTFS	FTPTFENEDD	MTAVYQEAIP
TAEELTLTGA	DIENGATMD	YWEALLKNTG	EAPLTTIKIK	PTATWAAGIG	APNTIFVQGT
GQNTKAFPVT	KEQWTTGAGV	SITLDQPLPA	GGQLKMNLLG	TAVTGNPSQV	LTADVEVTGN
FGSLTAKDTV	RIKDLDQEIT	SPDGDGFIST	PTDFGKLAI	SGSKQQKSLK	KAADYYNGGT
RNPYLRLNTS	QANWSLTAQL	SQPKSATDSL	PTTTRLLLCT	AAAASFIDYN	QPTETRTPLG
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VTGP					

EF107-3 (SEQ ID NO:415)

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GCTAGTGAAG	CGAAAACAGT	ACCGCCACAG	GAAACGGCAA	GAATTGCTTC	TCGAGCGATT
GGTTATTCTT	CTGTGGAAGG	GCGCGAGATT	CCCTTTTTCT	TTGTGDSASA	AGACGGGACG
TTGTTTGATC	CCGACCGAAT	TACGATGGCG	GTCAATCTTT	CCACGTTTTC	GTTTTATGAA
GAGAAATTAC	AACGAACCCC	CCTTGAGCCC	ACCACTGTGA	ATGGCGGAAA	GTTACTGTCT
ATTCCAACGT	CACCAGCTTT	TAAATATGAT	ACAAATAACC	AGAATCCGAG	TAATATTAT
GGCGTTTCTG	AAGTGTCGTT	TACTATTCTT	AAGGAGTATC	AAAGCCTGSA	CATTTCGACCA
AGTACGTTTT	ATACAGGAGA	CACTACGCAA	TATCCAGTGC	CAACGGTTTT	TGCGAACGTT
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GAAAAAATGC	CCAATAAGCT	GACGTTTGGT	CCTAAAAAGA	CGTTTAAATA	TACGGTAGCT
ACGGCACCAG	GAGGCGTTAC	GTATGCGCTG	ACCTATTTTT	ATGGAGATGT	CGGCGGTCCA
ACTAGTTCGC	ACCAAAGACG	AGGAACAGCG	GGTCCTGTGT	ATTATTATTT	AACAAAGCGG
CGTGTACCGG	AAAAATTTGA	GAATCCCGCA	GGCGGGGCGA	TTCTTGCGGC	AGAAGGTTAT
ACGCAGGATA	AGAAAACCAT	TGTAACAGGG	GAGGATTTTA	CTTTTACGSA	AGAAGGCACC
TTGCTCGAAC	GTTACACAGG	CAGTGATGGG	AAGACGTATT	TATTTAAAGG	TTGGTACAAA
GGGAATGCGA	AACCTAGCAC	GTTGGAAACC	ACCAAAACGC	CTAGTTATGC	GCTGACCTAT
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CCAGCGAGAG	AAGCTTTGTT	CGGCTATGTT	GATGAGCAAG	GAAACTTGAT	TAATCCCGCC
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CAAAAAGTCT	ACACACGCCC	AGACGATGGG	ACAATCGTAA	CTTATGCGGC	GCAAGAAGTG
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ATCACGCCAC	CAACTGGCTT	TACACAAGGA	AATCAGCTAG	TGGTGGACAG	TGAAAACATAT
GTCTACACTG	TCGCAAAAGC	TTTGCCGAAG	ATCTACCAAG	CTGGTGAAAA	AACCTATATC
TTCCAAGGCT	GGTTTAAAGG	CAAAACCAAG	CCAGCAACAT	TAAAGAGGAC	AACGACCCCA
AGTTTTACAC	CAACTTTTAA	TGATGAGGAC	GACATGACCG	CTGTGTACGA	AGAAGCGATT
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ACGGGTCAAA	ACACCAAAGC	TTTTCTGTCT	ACCAAAGAAC	AATGGACGAC	CGGTGCAGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGTCTATCA CBTGGATCA GCCTTTACCA GCTGGGGGTC AATTAAATAT GAATTATTA
 GGAACGGCCG TTACAGGAAA TCGTGGTCAA GTTTTAACCG CTGATCTTGA AGTAACGGGC
 AACTTTGGCA GTTTAACTBC CAAAGATAGG GTCTGTATTA AAGACTTTGA TGAAGAAATT
 ACGATCTCTG ACGGCGACCG CTTTATTAGT ACCGCGACAT TTGATTTTGG TAAGCTAGCA
 ATTTGAGGAA GTAAGCAACA ATATGGTTTG AAGAAGCGCG CAGATTCTA CGGCAATGGC
 ACTGCGAACC CTTATTTACG CCGTAATACT AGGGAAGGCA ATTGGAGCTT AACGCGCCAG
 CTATGCGAAC CAAAATCAGG CACAGACAGG TTGCGAAGAA CGACCGCTTT CTTGCTAGGA
 ACGGCGGCTG CTGCGAGCTT TACCGACTAT AAGCAAGGCA CAGAAAGAG GACAGCACTT
 GGCAAGAGCA GCACCGTAGT TTTAAGCGCG GACAATAGCG CAACAGCGGT CGTGGCAAAAC
 CAACAGTTCA CAGGCGAGTA CGTCTATCAG TTGCACTTCA CGTTTGTAA CATCAAACTA
 GAAGTCCGAG CCAACCAAGG TATGGTGGG CAACAATAGT AAGCGCGGT CAGCTGGAAT
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EF107-4 (SEQ ID NO:416)

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 SEAKTVPPQE TARIASRAIG YSSVESREIP FFFVEEDGTL FDPDRITNAV NLSTFSFYEE
 KLQRTPLEPT TVNGSKLLSI PTSPAFKYDT NNQNPENIYG VSEVSFTNPK EYQSLDIRPS
 TFYTGDDTQY PVFTVFANVG GKVTNIVGAN AETELELTNE KMPNKLTEGP FKTFPKYTVAT
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 DKTKYPVPNE VREGIENPDN IVSSLVGXXA YNLTQKSATR YTARRSYXW BPTKTLYSMS
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 FGSILTAKDTV FIKDLQDEIT SPDGDGFIST PTFDFGKLAI SGSKQQLNLE HAADYYGNGT
 RNPYLRLNTS QANWSLTAQL SQPKFATDSL PTTTRLLEGT AAAASFDMYN QPTETRTPLG
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 VTGP

EF108-1 (SEQ ID NO:417)

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 CAAGCAGAAG TGGAACAAGC AGAAACACCA ATCATTCTTA AACCAGAAAG AATCAATATG
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 GCGAGTCTCT ACAATAGAGA AGGTAAAATT GATTCTACTT ATCCGTIACC TGCTATTGCA
 CTAGCAGGTA CTAGACCGCT ATCTTTGACT CAAAGTAGTG TAATTAATGC ATGGCGGCTG
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 ATAGGTTATA AGACTGTGAG TAGCCCAATC TATTACCATC TGACCAAGCG CCGTGTCAAC
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 ACCTACAAAG TTGCGACGAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 TTCCAAGGTT GGTATAAAGG GAAAACCAAG CCAAGTACGT TGAACAAAC AACAACTCCA
 ACGTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATAA GGAAGAAATA
 CCAACAGCTA GTGTACATT AACTCCACCA AAAGAAGTGA TTGATAGCAA TACCAATGTA
 ATCTGGACAA CAACGATCAC GAATACTAGC AAAGCACCTT TACAAAATCT CACCTTGAAA
 AAAGGGCCCA ATTGGTCAGC TGGTCTGACG ATCCCGACCT TTATGGATGT GACACCAGAA
 GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTTT GGACAGATGG GGTTCCTTTA
 CCAAATGCCG TTCTATCGG CAAAAAGTT TCAGTTGCTT TCACAACTCG CGCAACAGGG
 AAACCAACA CTGTTTGAAG AGCAGAAGTT GTAGTATTTG GTGGTATTA AGATAGTACA
 GTGGATAACT TCGTGAGAAT TCGTCCAAAT GATCAAGAA TAGTCACAGC AACGACCGAA
 GGCTTCATCA GTGTGCCAAC CTTGCACTTC GGCCAAGTGG GCGTTGCAGG AACTAAGCAA
 CAACACAGCT TGAACAAGC CGCGGATTAC TACGGTAACG GCACACGAAA TCGGTATCTG
 CGGATTAAGA AAACGCAACC CAATTGGAGC TTAACAGCCG AACTGTGACA ACCAAAATCA
 GCGACAGACA GCTTGCCTAC AGCGACCCGC TTATTATTAG GGGCGGCGCG TGTCTCTAGC
 TTTACCAATT ACAATCAACC AACCGAGTTG AAAAATACCG TCGGTACGAC GAGTGCCATT
 AGCTTAACAG CCAACAACAC AGCAACGAGT ATTATTGCCA ACAAGCAAT CACAGSTAGT
 AATGTTTATC AGTTGGACTT CACCTTCAAT AATGTCAAAC TTGAAGTCT AGCCAATCAA
 GGTGTTAAAG GGCAACAATA CAAGGTCGCA GTTACATGGA ACCTAGTAC AGGTCTTAA

EF108-2 (SEQ ID NO:418)

MKQTKWQ RLATIGLCSS LVINAFSGVT AVAETVTIES SPTAESSAKF
 ETQASSVKEE TTKASTENSQ VTTDTSQEEA TKEAEKEEPQ AEVEQAETPI IFKPKINMK
 ATYSFSAETY QFGFVNESGQ LINPEIIPIT YSYAKGSWFT DGYNRKNTSM VQGSASTVGN
 LKNVIMPATS VVMPPGPSYE GTQEVYTNFS IRIPKYYASA SLYNREGTID STYPLPAIAL
 AGTRPLSLTQ SSVISALALT SKGENVYTPR ETFFGGDPAG VKFTNFLERI NDFDVKGNNI
 GYKTVSSPIY YHLTNRRVTE NFVETSGAKI TPPSNFTQSK QTVINSIDYT FQSGFLPET

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YKVGTKSYRF KGWYKSKTKT EPLATYKTPS YKNTYELNLD LTAAYEY ES VELPASTNQF
 GFIDEATNKL IAPDQVQMKY NLTFLNHNKK TMSSENLTST DIATLKN SV FNNYFEQYRV
 NTFYGASDIT FTLPKRYKSI NITPFLSKTE PAFPLPHIT IQQNEMKMP WTTYNKLKQL
 SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PNYNYTMSPP WYYYLENEM TENFVDTNGA
 KITPPTGFTQ GKKTIVITSDA YTFEJASTLP DTYTTGGHIF KFKGWTNKK IDNTLITTKA
 PSYQVITYDDN IELNAYVEEE TTTTYPSND MNFINENKDA FTPALTFNKK NYAQSTSAYL
 RTDLYDVTSK NNGNGQYTVS INNGSMPLSQ ELLKKYVINEQ PISATHNKKP NVOKLAIDQQ
 LKYVDSIQLD TAQSSNLKSY RYTYTNNSL VFDPNVAFAE VDLSSSEKSL INFDSGTYF
 SMANNRLFYT HLGYSSTPGV NYLLNMFLEN AKPADSKLV YKVTREKTE NFMDVNGAKI
 TAPTGTGTQN QVPMNSNTFK YTAARALPAT YTTGGKNTTF QGWYKGTNKP STLNKTTTPT
 FNATFD3NDD MTAMYKEEIP TASVTLTRPK EVIDTNTNFI WTTTITNTSK APLQNLTLKK
 GPNWSAGLTI PTFMEVTPFG ETTHSIPVNS TLWTEGVNIP NAVPIGNTS VAFTRATGK
 PNTVLKAEVU VFGGIKDSV DNFVIRIPND QEVVTPPTES PISVPTTFEG QVGVAGTKQQ
 HSLKQAADYY GNGTRNPYLK IKKTYPNWSL TAQLSQPKSA TDSLPTATFL DGAAPVSSF
 TNYNQPTCLK NTVGTTSAIS LTAINTATSI IANKQETSDN WYQLDFEEN EKLEVPANQG
 VKGQQYKAAV TWNLVGTG

EF108-3 (SEQ ID NO:419)

CGT GACGATTGAA AGTAGTCCGA CCGCGGAAAG TAGTSCCAAG
 GAAGAGACGC AAGCAAGTAG CGTCAAGGAA GAAACAACCA AAGCCATAG GGAATAAGT
 CAAGTAACAA CTGACACGAG TCAAGAAAGAA GCAACGAAAG AAGCGGAAA AGAAGAACCG
 CAAGCAGAAG TGAACAAGC AGAAACAACA ATCATTCCTA AACCAAGAAA AATCAATATG
 AAGGCAACTT ATTCATTTTC TGCAGAAAAT TATCAGTTTG CATTTGAAA TGAATCAGGT
 CAATTAATAA ATCCAGATAT TATACCAATT ACGTATAGCT ATGCCAAGG ATCATGGAAG
 ACAGATGGTT ATAATCGAAA GTGGACTAGT ATGGTTCAAG CGAGTGTCT AACCGTAGGA
 AACTTAAAGA ATGTAATAAT GCAAGCAACT TCTGTAGTCA TGCCACGAGG AAGGTTCATAT
 GAAGGAACCT AAGAGGTGTA CAGAAACTTT TCAATTGCGA TACCAAGATA TTATGCATCA
 GCGAGTCTCT ACAATAGAGA AGATAAAAT GATTCTATCT ATCCGTGAGG TGTATATGCA
 CTAGCAGGTA CTAGACCGCT ATTTTTGAAT CAAAGTATG TAATTAGGCT ATTTGGCGCTG
 ACCAGTAAAG GAGACAATGT TTATACACCA CGGGAACAT TTTTTSAGG AGATCCTGCA
 GGTGTAAAGT TACTAATTT TTTGTATCGT ATAAATGACT TTGATGAAA AGTAATAAC
 ATAGGTTATA AGACTGTGAG TATCCCAATC TATTACCATC TGACCAAGCG CCGTGTACAC
 GAAAACCTTCG TAGATACAAG TGGGCGCAAA ATCACGCAAC CAAGTAAATT CACCCAGGG
 AAACAAACGG TCATTAACAG TGATCCCTTAC ACGTTCDAAC AAAGTGCTTT TTTACCCGAG
 ACCTACAAAG TTGGCACGAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCAAA
 ACCGAGCCTT TGGCCACCAC TAAAACACCT AGCTATAAAG TCACGTATBA TACAAATGAT
 GATTTGACGG TGGTCTATGA GGAGTTTTCA GGGTACGAGC TGCCTGTCTC GACCAATCAA
 TTTGGCTTTG TGGATGAAGC GACGAACAAA TTAATTGCTC CCGACCAAT GCAGATGAAG
 TATAATCTTA CTTTAAATGA AAATAATAAA AAAACAGTAA TGAGCACTAA CTTAACGGGG
 ACAGATACAG CGACACTGAA AAATTTGTCC GTGCCTGTCA ACTATTGTA ACAATATCGC
 GTCAATACGT TTTATGGCGC GAGTGAATTT ACGTTTADAT TGCCCAAGCG GTACAAATCA
 ATCAATATTA CCAAAATCAGA TGGCAAAACG GACCCAGCTT TTCTCTCTCC TAAAATCTAT
 AATATAGATC AAGTAGAAAT GTCAATATG CCTGTGACTA CTTATAAGAA GTTGAAACAG
 CTGTGGGGCC AACGTTTGG CTTAATGTCT TTAGCCGATC AACCTGAATT TTATACGAAA
 ACGTTATTTG GGACAGAGTC TGGTATGAT GACCCAGTCA ATTATTATAC AATAGTGGC
 CCTGTTTACT ATTATTTAGA AAATCGGAAA GTCACCGAGA ACTTCGTAGA CACCAACGGC
 GCTAAATCA CACCGCCAAC AGSTTTTACC CAAGGTAAAA AAACGGTAT TACAAGCGAC
 GCCTACACTT TCAACAAGC AGGCACCTTA CCAGACACTT ACACAAGAGG CGTAAGACC
 TACAAGTTCA AAGGTTGGTA CAAAGGCAAG TCCATAGTCA ACACATTGAC AACTACCAAA
 GCGCCAAGTT ATCAAGTGAC CTACATGAC AATGATGATT TGAATGTCT GTATGAAGAA
 GAAACAGTTA CGACAGTGTA TCCATCAGTC GATATGAAT TTGTGAATBA AAAAGGCGGG
 GCTTTACAC CCGCGTTAAC TTTTAGTGT AAGTACTATG CGCAAAGTAC GAGTGGGTAC
 TTAAGAACCG ATTTATATGA CGTACCTCA AAAAATAATG GTAATGACA ATATACGGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGTATTAATA ATGGTAGTAT GGCATTGTCC CAAGAATTAT TGAAAAATA TAATAATGGA
CAACCAATCA GTGCTACCAA CAGATTACAG TTTAATGTTG ATAAATAGC CATCGACCAA
CAACTAAAT ATGTTGACAG CATTGAATTA GACACAGCTC AAAGTAGCAA TGTGAAATCC
TATAGATATG TGTACACGAA CAATAGATCA CTGTTTTCG ACCCAATGT AGSACCAGCA
GAGGTTGACC TTAGTTCAGA ATCTTTTAC TGTCTTAATT TTGATTGAG TGGCACCCTAT
TTTTCTAATG CAAATAATAG ACTTTTCTAC ACGCATTTAG GATATATGG CACACCAGGA
GTTAACTATC TTCTCGTAAT GTTTTCTTTT AACGCCAAAC CTGCGGATAA GTCAAAACTT
GTCTACAAAG TCACTCGCAA ACAAGTCACC GAAAACCTG TGGATGTCAA CGSTGCCAAA
ATCACTGCAC CAACAGGCTT CACCTAAGGT AACCAAGTAC CAATGALCA3 TAACACCTTC
AAGTACACAG CGGCAAAAGC TTTACGACG ACGTATACTA CAGGTGTCAA AGTCTATACG
TTCCAAGGGT GGTATAAAGG GAAAACCAAG CCAAGTACCT TGAACAAAC AACAACTCCA
ACGTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATTA GSAAGAAATA
CCAACAGCTA GTGTCACATT AACTGACCA AAAGAAGTBA TTGATAGCA TACCAATGTA
ATCTGGACAA CAACGATCAC GAATAGTAGC AAAGCACCTT TACAAATGT CACCTTGAAA
AAAGGGCCCA TTGGTTCAGC TGGTCTGACG ATCCCGACCT TTATGCAAT GACACCAGAA
GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTTT GGACAGAG33 GTTCTCTTTA
CCAAATGCCG TTCCTATCGG CAAAAAAGTT TCAGTTGCTT TCACAAAT33 CGCAACAGGG
AAACCAACA CTGTTTTGAA AGCAGAGTT GTAGTATT33 GTGGTATTAA AGATAGTACA
GTGGATAACT TCGTGAGAAT TGGTCTAAT GATCAAGAAG TAGTCAAC3 AACGACCGAA
GGCTTCATCA GTGTGCCAAC CTTCGACTTC GGCCAAGT33 GCGTTCGAG3 AACTAAGCAA
CAACACAGCT TGAAACAAGC CGGCGATTAC TACGGTAA33 GCACACG3AA TCGTATCTG
CGGATTAAGA AAACGCAACC CAATT33AGC TTAACAGC3C AACTGT33CA ACCAAATCA
CGCAGACACA GCTTGCCCTAC AG33A33CGC TTATTATT33 GGGCGG3333 TGTCTTAGC
TTTACCAATT ACAATCAACC AAC33AGTTG AAAAATAC33 TCGGTAT33C GAGTGCCATT
AGCTTAACAG CCAACAACAC AG33A33AGT ATTATTG33A ACAAGC33ATT CACAGGTAGT
AATGTTTATC AGTTGGACTT CAGCTTTAAT AATGTCAAAC TTGAAG3333 AGCCAATCAA
GGTGTAAAG GGCAACAATA CA4333CGCA GTTACATG3A ACCTAG33TAC AG

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EF108-4 (SEQ ID NO:420)

VTIES SPTAESSAKE

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ETQASSVKEE TTKASTENSQ VTTEISPEEA TKEAEKEEFQ AEVEQAETFI IPKPKKINMK
ATYSFSAETY QFGFVNESGQ LINFDIIPIT YSYAKGSWKT DGYNRFWTSM VQGSASTVGN
LKNVIMPATS VMPPPGPSYE GTQEVYTNFS IRIPKYYASA SLYNREKID STYPLPAIAL
AGTRPLSLTQ SSVISALALT SPGBNVYTPR ETFFGGDFAG VKFTNPLYFI NDFDVKGNNI
GYKTVSSPIY YHLTNRRVTE NEVETSGAKI TPPSNFTGCK QTVINSTPYT FQQSGFLPET
YKVGTKSYRF KGWYKGKTKT EPLATFTTPS YKVTYDDNDD LTVVYENFEG YELPASTNQF
GFVDEATNKL IAPDQVQMKY NLTLENNKK TVMSSNLGCT DTATLENL3V PVNYFEQYRV
NTFYGASDIT FTLPKRYKSI NITYSELKTD PAFPLPKLYN IDQVEN3MP VTTYNKLKQL
SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PVNYYTMSGP VYYYLEN3KV TENFVDNNGA
KITPPTGFTQ GKKT3VITSDA YTFPQAGTLP DTYTTGGFTY KFKGWY3GKS ILNLT3TTKA
PSYQVTYDDN DDLNVVYEEE TWTTVYF3VD MNFVNEK3GA FTPALT3GK YYAQST3AYL
RTDLYDVTSK NNGNGQYTVS INNGSMPL3Q ELLKKYNI3Q PISAT33LQF NVDKLAID3Q
LKYVDSIQLD TAQSSNLKSY RVYTHH3SSL VFDPNVA3AE VDL3SE33NL LNFDSDGTYF
SNANNRLFYT HLGYS3GTPGV NYLLVMFLFN AKPADK3FLV YKVTRK33TE NFVDVNGAKI
TAPTGFTQGN QVPMNSNTFK YTA33ALPAT YTTGGKV3TF QGWYKG33TF STLNKT33TPT
FNATFDGND MTAMYKEEIP TAS33L3TRPK EVIDTNT3VI WTTTIT33TSK APLQNL3LKK
GPNWSAGLTI PTFMEVTP3G ETT33IPVNS TLWTEGV3PL NAVPIG33VS VAFTRAT3K
PTNVLKAEVV VFGGIK3STV DIF33IRPND QEVVTP3TEG FISVPT33LG QVGVAG33KQ
HSLKQADYY GNGTRNP3YL IFKTQ33NWSL TAQL33Q33SA TDSLPT33TEL LLGAAP33SSF
TNYNQPT3ELK NTVGT33AIS LTANT33T3SI IANKQ33TGSN VYQLD33TENN VFLEVPAN3Q
VKGQ33YKAAV TWN33LVT

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EF109-1 (SEQ ID NO:421)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

AGGAGTAAAT TAATGAAAAA AATTTTATA ACTAGTTTAA TGTAG AGT TTTGTTGTCTG
 GGATTTCTGG TTACCCCTAT TTCTGTTTAC GCTTTTGAAG CCTCTATGGG AACTACTGAA
 GAAACGGTGG CTTGAGAAAC ATCTTTAAGG GAGCGACAAA TGAGTATGGG TTTCACTGAA
 GAAATGAACC CAACCATCAT AAATTCTCAA GAGGAAACAG AAACAA CTC CACTTCTCTCA
 ACCTCCGATT CCACCACTGA ACTTTTACA TCAGAAAGTAA CAACTCTTAA TATACAGAA
 NATAGTAGGG AGTACTGAA ACTATTTTGG NAACATCAAT AAGTAA AGG GAGACACCTA
 TAG

EF109-2 (SEQ ID NO:422)

MKKSVI TSSMLAVLLS GFLVTPISAY ALERSKOTTE ETVAGETSLT ERQMSGGVTE
 EMNPSIINSQ EETETTSTSS TSDSTTEVST SEVTTTNTTE KSSDVLKLDL NHHXVMRTHL

EF109-3 (SEQ ID NO:423)

GGAAC GCTCTAAGGG AACTACTGAA
 GAAACGGTGG CTTGAGAAAC ATCTTTAAGG GAGCGACAAA TGAGTATGGG TTTCACTGAA
 GAAATGAACC CAACCATCAT AAATTCTCAA GAGGAAACAG AAACAA CTC CACTTCTCTCA
 ACCTCCGATT CCACCACTGA ACTTTTACA TCAG

EF109-4 (SEQ ID NO:424)

ERSFGTTE ETVAGETSLT ERQMSGGVTE EMNPSIINSQ EETETTSTSS TSDSTTEVST S

EF110-1 (SEQ ID NO:425)

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 AGTGCTGGTT TTTCTTTTCT GATTTTACTA AATTTGATAG GCGGTTTATG TTGCTCTGCA
 AATGCAGAAG AGTATATCGT TCCTGCGGAA AGTCATTGAC GACAAAAAAG ATCGTTACTG
 GACCCGTAGG ACAGAAGACA AGAAGTGGCA GATACAACGG AAGCGCTTTT TGGGTCAATC
 GGAAGAATCA TTTCCCTGTC CAGTAAGACA GGCTATATTT CTTTAGGAAC AAGCTTTGTT
 GTTGAACCA ATACAATTGT CAGCAATAAT CATGTGGGAG AAAGTTTCAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTATC CAGGTGAGGA TGGCAGTGCG
 ACACCATTTG GCAAATTCAA AGTGATGAT GTAGCTTTTT CCCCAGATGC GATATTGCG
 GTAGTGACTG TCGGCAAAACA AAACGATCGT CCAGATGGCC CAGAGTGGG AAAAAATTTA
 ACGCCATTTG TTTTAAAAA GTTTGAATCT TCAGATAGCC ATGTCAAAAT ATCAGGCTAT
 CCAGGTGAGA AAAACCAAC ACATGATGCT CATGAAAATG ATTTGTTTAC ATCTAATTTT
 ACAGACTTAG AAAATCCATT ACTATTTTAT GATATGATA CAACCGTGGG TGAATCTGGT
 TCACCAATCT ATAATGATCA GGTGGAAGTA GTTGGTGTTC ATTCCAGTGG CAGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGAATT ATAATTAT TGTTAATCGA
 GTGAATGAAG AAGAAAAATA AGGTTTATCC GCTGTGCGAG CAGCGTAA

EF110-2 (SEQ ID NO:426)

MKKFSIRKIS AGFLFLILVT LIAGFSLSAN AEEYIVPAES HSRQKRLLD
 PEDRRQEVAD TTEAPFASIG RIISPAKPG YISLGTGFIV GTNTIVTINH VAESFKNKV
 LNPNAKDDAW FYPGRGSAT PEGHFYVIDV AFSPNADIAV VTGKQNDRP DGPGLGEILT
 PFVLKFFESS DTHVTISGYP GEKNHTQWSH ENDLFTSNFT DLENPLFYD IDTIGGQSGS
 PIYNDQVEVV GVHSNGGIQ TGNHGFRLNE VINYFIVNEV NEEENKLSA VPAA

EF110-3 (SEQ ID NO:427)

AG AGTATATCGT TCCTGCCGAA AGTCATTAC GACAAAAAAG ATCTTACTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACCCTGAGG ACAGAAGACA AGAAGTGGCA GATACAACCG AAGCGCCTTT TGGCTCAATC
 GGAAGAATCA TTTCCTCTGC CAGTAAACCA GGCTATATTT CTTTAGCAAC AGGCTTTGTT
 GTTGGAACCA ATACAATTGT CACCAATAAT CATGTGGCTG AAAGTTTAA SAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTTAT CAGGTGAGAG TGGCAGTGCG
 ACACCATTTG GCAAAATCAA AGTGATGAT GTAGCTTTT CCCCGAATGC GATATTGCG
 GTAGTGACTG TCGGCAAACA AAAGGATGCT CCAGATGGCT CAGAGTTGGG AGAAATTTTA
 ACGCCATTTG TTTTGAAAAA GTTTGATCT TCAGATACCG ATGTCACAAT ATCAGGCTAT
 CCAGGTGAGA AAAACCACAC ACAATGCTCT CATGAAATG ATTTGTTTAC ATCTAACTTT
 ACAGACTTAG AAAATCCATT ACTATTCTAT GATATGATA CAACCGGCGG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTTGAAGTA GTTGTGCTT ATTCCAATGG CGGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGATTA ATAACCTTTAT TGTAAATCGA
 GTGAATGAAG AAGAAAAATA ACSTTATCC GCTGTGCGAG CAGCGT

EF110-4 (SEQ ID NO:428)

EYIVPAES HSRQKRSLLD

PEDRRQEVAD TTEAPFASIG RIISPAKPKG YISLGTSEVV GTNTIVTNHH VAESEKNAKV
 LNPNAKDDAW FYPGRDGSAT PFGKPKVIDV AFSPNADIAV VTGKQND RP DGPGLGEILT
 PFVLKKFESS DTHVTISGYP GEKNHTQWSH ENDLFTSHFT DLENPLLEFYD IDTTGGQSGS
 PIYNDQVEVV GVHSNGGIKQ TGNHGGRLNE VNYNFIVHEV NEEENKELSA VPAA

EF111-1 (SEQ ID NO:429)

TGATCAATAC ACTTCGATAC GGTGCGCTTT TTTCTAGAGA AAGTTGAATC TTTCAATAAT
 AAAAAGGGAT ACACCTCCATT TGGCATAGTC CTTGCTGATA ATAAATCAGT GTATAAAGCG
 CTATCATTTT ATAGGAGGGG TTTTATGAAG GGTTTATCAA AAAAGAAACG GGTGCTACT
 TGGTTAGCGT TAGGAATCAC CGTAGTCAGC TGTTTTGCGT TAAGCAGGGA AGTGCAAGCA
 AGTGTGAA GAACAAAAGT TGATGAATTT GCAATGCTT TAGATGTGAG TGCATCACCA
 ACCGAACGGA CGAATGGCGT ATACGATACC AATTATTTTA ATAATTTTTC TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATAAAG AGCTACTGGG TGGTTTGGCG
 GGGCCATTGA TTATTGCGGA AGAATATCCA GTAACTTCG CGGCAACTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGGAGAAACC TATGATTAA GCCAAAGCAA CCGCATGGAC
 CTGTCTTATT ATCCTGGGCG CCTAGAGCAA ACCTATGAAT TAGACGATT AACGATTCAT
 TTAGCTTTAA TTTTGTGAG CAATCGAAGC GCGCTTATCC AAACGACACT TGAAACACT
 GGTGAAGAGC CCTGTGCACT TGGAGCAAGC TGGACAGTGG CGGTCTTTGA CAAAATTCAA
 GAGGGAACGG AAACCTTAGA TATTGGGACT CGTTTAACTG CTAAAGACAA TGACATTCAA
 GTGAATTTTG GTGAAGTCAG AGAAAGCTGG AATTATTTTG CTACGAAGA CACAAAATAT
 ACGATTCATC ATGCGGATAA AGTTTCAACA AAAATTGATA ATCGGAATTA TACAGCAACC
 GCTGAACCAA TTGAATTGAA GCCTAAACAA ACGTACAACA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAAAGAA CAACAACAAB CACCCGATA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAABCAA AGATGGCAAB GATATCTAGA TAAACGTTT
 GATCAAAAGA AAACAGCAGA ATTTCTTGAA TATCAAAAB CGCTAGTCAA ATCGATTGAA
 ACGATTAAATA CCAATTGGCG AAGTGCGGCA GGTGCTTTA AGCATGACGG GATTGTCCG
 TCCATGTCTT ATAAATGGTT TATTGSTATG TGGGCTTGGG ATTCTGTGAA AGCGGATGTA
 GCAACGGCTG ATTTTAATCC TGAGTTAGCT AAAAATAATA TGCGGGCTT GTTTGATTAT
 CAAATTCAAA AAGATGATAC CGTACGTCCA CAAGATGCAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC CGGTGGTGGT GAAGGTGGCA ACTGGAATGA ACGAAATCTT
 AAACCACCAT TGGCTGCATG GGCAGTTTGG CATATTTATC AAGAAACCAA AGATAAGGAA
 TTTTAAAAAG AAATGTATCC CAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGAATAT GGAAGCATGG TTAGTGATGC TCACTGGCAA
 AAAGACGACA AGGATCAAAT CATTAAGAT AAAAATGGCC ACTAAATG CATGATGATG
 CTGTTATTGA AGCAGCCGCG TGGGAAAGTG GCATGGATTA CACTACCGG TTTGACAAAG
 AAGGTGTGGG CAAAGCGGAC GTTGGAGTTA AAGTTTTTGA AAACAAAAT AAAGGAAAAG
 TAG

TABLE 1. Nucleotide and Amino Acid Sequences of *Alcaligenes* Genes

EF111-2 (SEQ ID NO:430)

MKS LSKKKRVSTW

LALGIVTVSS FALSREVQAS VERTWIERFA NLELWFAHLL ERTNGVYDTN YFNNFSDLGA
 WHGYLPEKS NKELLGGFAG PLIIAREYVP NLAASLNHIT YFNKKTSETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLNHT EEPLESLGASW TGAVFDFKIQE
 GTETLDIGTR LTAKNDNIQV NFEVRETWN YFATKDTHTT IHHADKSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEBAKEQ QQAPEYTHNA ARYFKENKQR NQGYLDKTFD
 QKKTAEFPEY QNALVFSIET INTNWSAAG AFKHGCGINT MSYKWFIMN ANDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGALIDANF YHQDSAFSGE GSNWERNNSK
 PPLAAWAVWH IYQETKDFEF LKEMYPHLVA YHNWYTHED HUKNGIAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMMLL LLKQPRSKVA WITLHGLTHK WKAKATLELK FLKTHIKEK

EF111-3 (SEQ ID NO:431)

TGATGAATTT GCAAAATGTTT TAGATGTGAG TGCATCAGCA
 ACCGAACGGA CGAATGGCCT ATACGATACG AATTATTTTA ATAATTTTTC TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATANAAG AGCTACTGSS TGGTTTTGCG
 GGGCCATTGA TTATTGCGGA AGAATATGCA GTAAACTTSS CGGCAAGTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGAGAGAAAC TATGATTTAA GGCAAAACAA GGGCATGGAC
 CTGTCTTATT ATCCTGGGCG CCTAGAGCAA ACGTATGAAE TAGACGNTT AAGGATTCAT
 TTAGCTTTAA TTTTGTGTCAG CAATGAAAG GCGCTTATCT AAAGGAGACT TGAAAAACACT
 GGTGAAGAGC CTTTGTCACT TGGAGTAAGC TGGACAGSTG CGSTTTTGA CAAAAATCAA
 GAGGGAACGG AAACCTTAGA TATTGGCACT GCTTTAATG CTAAAGACAA TGADATTCAA
 GTGAATTTTG CTGAAGTCAG AGAAAGCTGG AATTATTTTC CTAGGAAAGA CACAAAATAT
 ACGATTTCATC ATGCGGCATAA AGTTTGAACA AAAATTGATA ATGGGATTTA TADAGCAACC
 GGTGAACCAA TTGAATTGAA GCCTAAGCAA ACCTACACCA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAGGAA CAACAGDAAG CACCGGANTA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAAGCAA AGATGGDAAG GATATGTABA TAAAACGTTT
 CATCAAAAAGA AAACAGCAGA ATTTCTGAAA TATCAAAAAG CGCTAGTCAA ATGATTTGAA
 ACGATTAATA CCAATTGGCG AAGTGGGACA GGTGCTTTTA AGCATGACGG GATTGTTCCG
 TCCATGTCTT ATAAATGGTT TATTGCTATG TGGGCTTGGG ATTGCTGGAA ACGGATGTA
 GCAACGGCTG ATTTAATCC TGAGTTAGCT AAAAATAATA TGGGCGCTT TTTTGATTAT
 CAAATTCAA AAGATGATAC CGTACGTGCA CAAGATGAGG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC GCGTGGTGGT GAAGGTGGCA ACTGGGATGA ACGAAATCTT
 AAACCACCAT TGGCTGCATG GGCAGTTTGG CATATTATAT AAGAAACCAA AGATAAGGAA
 TTTTAAAG AAATGTATCC CAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGATAT GSAAGCATG TCAGTGATGT TCACTGGCAA
 AAAGACGACA AGGATCAAAT CATTAAAGAT AAAAATGGG ACCTAAGTG GATGATGATG
 CTGTATTGA AGCAGCGCG TGGGAAGTG GCATGGATTA CCTACACGG TTTGACAAAG
 AAGGTGTGGG CAAAGCGCAC GTTGAGTTA AAGTT

EF111-4 (SEQ ID NO:432)

DEFA NVLDVSASPT ERTNGVYDTN YFNNFSDLGA

WHGYLPEKS NKELLGGFAG PLIIAREYVP NLAASLNHIT YFNKKTSETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLNHT EEPLESLGASW TGAVFDFKIQE
 GTETLDIGTR LTAKNDNIQV NFEVRETWN YFATKDTHTT IHHADKSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEBAKEQ QQAPEYTHNA ARYFKENKQR NQGYLDKTFD
 QKKTAEFPEY QNALVFSIET INTNWSAAG AFKHGCGINT MSYKWFIMN ANDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGALIDANF YHQDSAFSGE GSNWERNNSK
 PPLAAWAVWH IYQETKDFEF LKEMYPHLVA YHNWYTHED HUKNGIAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMMLL LLKQPRSKVA WITLHGLTHK WKAKATLELK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF117-1 (SEQ ID NO:433)

TAATTCGATG GAGAAGGTGG TTTAGTGAAG AGATTTCGAT TTTTCTTACT AATTTTACTT
 GCTTTAACAG GTTGTAATC CGGTGAAAAA GAATTTCGAT AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGCTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GCAGATTGTT GAGAGTGACA GTCTGTTCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ATAGTTTACG GAGAATATTA CGGCTTTTGT
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTACG CCACGAATTA G

EF117-2 (SEQ ID NO:434)

VKR FSFFLLILLA LTGCKSGEKE FDEESLQNLK ETXQXSETE LQNGDVRLNE
 YISLKGEIVE SDSRSSLIKK GDRFILKSGS SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK
 GTLIESEENH DSATN

EF117-3 (SEQ ID NO:435)

TG AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGCTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTCTGTTCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ATAGTTTACG GAGAATATTA CGGCTTTTGT
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTACG CCACGAA

EF117-4 (SEQ ID NO:436)

EESLQNLK ETXQXSETE LQNGDVRLNE YISLKGEIVE SDSRSSLIKK GDRFILKSGS
 SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK GTLIESEENH DSATN

EF118-1 (SEQ ID NO:437)

TGAGGGGGAA AAAGTGTGTT AAAAAGAAAA GTGGGGATTT TGCAGGCGT TTTCTGTCA
 GCTTTTCTTAC TGACAGGTG TGGCAAAAGT GCGAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCAATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CTTATGATTT GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTTCTGG GGAAGATTCA ATAGATGCG AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GATGTATGCG ATTTCAATGG TTGGATCGTT
 AGATAA

EF118-2 (SEQ ID NO:438)

VLKRKV GIVAGVFCSA LLLTGCGKSA KDEFIQIGIK XHAQESGVXD FMSISDMKF
 SQEDGAQTNP MIGMLITQIK DASLSCEDSS RQQRKSIQL RDEIKSDGN3 CTDFIGWIVR

EF118-3 (SEQ ID NO:439)

GAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCAATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CTTATGATTT GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTTCTGG GGAAGATTCA ATAGATGCG AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GATGTATGCG ATTTCAATGG TTGGATCGTT
 AGAT

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TABLE 1. Nucleotide and Amino Acid Sequences of E. tricus genes

EF118-4 (SEQ ID NO:440)

KDEFIQGIGN XNAQESGVXD FMSISDMKF SYEDDAWNP MISMILQIK DASLSGEDSS
 KCQKRKSIQL RDEIKSEBNG CTDPIQWIVR

EF119-1 (SEQ ID NO:441)

TAAAGAATAC CGAGTAAAT TTTGGGAAGC CTTTTTTTAA AAAATTGTAT ATGCAAAAGA
 AGTGCAACGG AAGGAGGCTC GGAATGCTG AATAAGGTA CTTTACTTAT TTTATTGTTA
 GGCAGAGTGT TGCTTGTTAG TGGCTGTCAA AGCATAAG AAGAAACAA GTCTAGTAAA
 GTATCGACAG AAGAAACGAC AGTGATTGAA ACASTAGCAA GGAACAATC GAAGGAATCG
 TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAAGA AATTAGAAGA ACCAGATCAT
 GTAAACTTTC TAGAAGCTTA TGGAAATGCG TATGGGAAT TTACAAGTAT TAATGATCGC
 AATGAAAAGC TAAAGCCCCT CATGAGTGAA AATGTATCA AAAAAAATGG AATTGATGTT
 AAAACTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTAGAA CATTATATAA AATGATCAA
 CATGAATATG CTTTACTTTT GGATTGTGAA CAAATGGA CACAGACACG AGTGTTACTT
 TTGGCTAAGG TGAAGAACAA TAAATTTCT GAAATGAGT ATAATTGAGT TAAGCAAGAG
 TATTAG

EF119-2 (SEQ ID NO:442)

VN KLPLLILLG GVLLVSGCQS HKEENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE
 TTKLEEDPHV KLEAYGNAY ANFTSINDRN EKLKPLMTEK CIKKNIGDVK TGVALVSVGK
 VTTIYKNDQH EYALLDCEQ NGTQTRVLLL AKVKNNKISE MTYNSVKQEQ

EF119-3 (SEQ ID NO:443)

AGAAAACAA GTCTAGTAAA
 GTATCGACAG AAGAAACGAC AGTGATTGAA ACASTAGCAA GGAACAATC GAAGGAATCG
 TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAAGA AATTAGAAGA ACCAGATCAT
 GTAAACTTTC TAGAAGCTTA TGGAAATGCG TATGGGAAT TTACAAGTAT TAATGATCGC
 AATGAAAAGC TAAAGCCCCT CATGAGTGAA AATGTATCA AAAAAAATGG AATTGATGTT
 AAAACTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTAGAA CATTATATAA AATGATCAA
 CATGAATATG CTTTACTTTT GGATTGTGAA CAAATGGA CACAGACACG AGTGTTACTT
 TTGGCTAAGG TGAAGAACAA TAAATTTCT GAAATGAGT ATAATTGAGT TAAGCAAGAG
 TAT

EF119-4 (SEQ ID NO:444)

ENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE TTKLEEDPHV KLEAYGNAY
 ANFTSINDRN
 EKLKPLMTEK CIKKNIGDVK TGVALVSVGK VTTIYKNDQH EYALLDCEQ NGTQTRVLLL
 AKVKNNKISE MTYNSVKQEQ

EF120-1 (SEQ ID NO:445)

TGAATAGGCG TGAAAAAGGG AATGTTAGCG TTTTTCCTG TCCTAGCGGT TTTATCATTA
 ACTGCTTGTC GGAACCAAAA AGNAAAGAAA GTAACCGGTT CAACGGAGGC ATCCTCTAAA
 GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAAAGA ACAAGCGAGC
 AGCAGTGTCT AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGCTGA TGGAAACAAT
 AGTCAGCTAA CTGTAGCTGA TTTAGATACT ACAGCGATTA ATGCTGGGCA TTTTACTACT
 TTAGTTGGAA TATGGAAAAA TGGTAAGGA GAGAGTTTGA TCATTGATCC TGATGGTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTGGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GGTGCGCTAT TATTATATAA AATTGGTGTT

EF120-2 (SEQ ID NO:446)

VKKGMLAF FVVLAVLSLT ACREPKKKKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNEKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF120-3 (SEQ ID NO:447)

AAGAAA GTAACCGCTT CAACGGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAACGA ACAAGCGAGC
AGCAGTGTGC AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGGTGA TGGAAACAAT
AGTCAGCTAA CTGTAGCTGA TTAGATACT ACAGGATTA ATGCTGGCGA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAAGGA GAAATTTGA TCATTCTATC TGATGGTAGT
ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTGGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GGTGCGCTAT TATTATATAA AATTGGTGTT

EF120-4 (SEQ ID NO:448)

KKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNEKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF121-1 (SEQ ID NO:449)

TGAAACACAA GGAGGAAATT TGTGAAAAAG TTGAGCTTAA AAAAAGTGAA GTGGGGCATG
CATT'TTTTAA TGGCTGTTGC GTTGATAGCG CCAAGTGTTA CTAGTACGGC ATATGCAGTA
GAAACAACGA GTCAACAAAG TTCAGAAGCA GTAACTAAGTA CCACCGATTG AAGTAGAAAA
AAGAACCAG TCATTACACA GGAAACAACA GATATCAAGG AAGAAGCACC AAATCAGGCT
ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCAGAGGCG CACACAGAGC GACGAATTTA
GAAACGTCAA TCGCTGAAAA AGAAGAAACG ACCAGCGGCG AAAAAATAAC AATTTTAGGT
ACGTCAGATG TTCATGGTCA ATTATGGAAT TGCTTTATG AAGATGATAA AGAACTACCA
GTTGGTTTGT CCAAGTAAG TACAGTCGTT AACCAACTCC GGGCACAATA CCCAGCAGGC
ACCGTTTTAA TTGATAATGG CGACAATATT CAAGGCACTA TTTTAACAGA TGACTTGTAT
AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCAATGA TCACCGCCAT GAATGTGATG
AAGTATGATG CAATGGTTTT GGGAAATCAT GATTTTAAAT TTGGTTTACC GTTAATCAAA
AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGCTTACGA ATACCTACAA TAAGGAAGAT
GGTCTTCGTT TTGTTGAAGG GACTACCAG AAGGAAGTTG ATTTTAATCA AGATGGGCAG
CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCCCG ACATTCCCTT GTGGGATGGC
CCTCGTGTTA CTTGCTTAA TTTTTTACCT TTGAAAAGG AAGCAGAAAA AGCAGTTACT
GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTGCTT CGATTCTATG GGGACAACAA
AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATGTCGCTGG GATTGATGCG
TATATTCTGG GTCATGACCA CCTTCTTTT ACCAAGIAG GAGCAGGCCC GAATGGAAAA
ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAAAG TTGTCAAAAT TGATCTTTCA
GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAAGTA CAGCAACGAT TGTACCAACA
ACGAATGTTT CAGCAGATGA AGCAGTTAAG GTAGTGACAA AAGAATACCA TGAAAAAACG
CGAGCGTTTA TTCAGGAGGA GATCGGCACA GAAACAGCTG ATTTTTTACC AAAACAAGAA
ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTTCTTT AATTAATAAC
GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGGGCGAG CGCTGTITAA ATACCACAGT
AAATTACCTG CGGGGAAGAT TTCCTATGCC AGGATTTTTG ATATCTACAA ATACCCGAAT
ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG

TABLE 1. Nucleotide and Amino Acid Sequences of *Maculalis* Genes.

GCGTACTATA ACCAAACACA GGCAGATGAT TGAATATGAT GTTTATATCG AAACATTCTGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GATTAAGAT GTGACATCTG AAAACCCAGTG
 GGTGAACGAA TTGTAGATGC GAAATTTGAT GATTAAGAT TGAATCTCTG CAAAGAATAT
 AGGATTGCTA TGAATAATTA TGCTTACGCG GCTTATATGA GCGAAGGAT TGAAGTAGGG
 GAACCTATTA AAAATTCTGA TGCAGAAAGC TTATGATATG GATTTCTGCA TTATATTAAAG
 AAAAAAGGAA CTCTTGATCG ABAACAAGAA ATTAAGATAT ATTGGTGAAT TATTGGGACA
 AATTTTGATG AAAAATGCGG TGCAGAAAGC ATTAAGATAT TGAATGATGG CACTCTTCAA
 ATTCGCACTT CTCTTGATGG AATTAAGATAT TATTAATTA AAACAAGATGTC
 CGTAATGCGG GCTTTGATTT AGATAATGCA TATACCATTA TGCAGAAAGC TGAAGTTTCAT
 GGTGACTAG AAGTAGGAGAA AGGCGAATTA GGTATGCGAT GGTAAAGAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGATGCA GCGGATCTTT TCGAAGGATC ACAAATCTCC
 AATTTCTCCA AAGGCGCGGA TATGCGCAAA GCAATGATAT AAGTTGCTTA TGAATGATG
 GCGGTGGGAA ATCAGGAGTT TGATTTTGCT TTAGAGATTA TACTAGCTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATG TAATTAATAG TATTAGAAAG ATGGGATGCG AGGGTTTTTT
 GATCCGTATA CAATCGTACA AAAATCGCGG AAAAAATCTG GAATTTCTG TGTGACGACC
 CCAGAAACAG CAATGAAAGC ACACCGGAAA AAGTATATTA AGGTGATAT TAAAGACCCG
 ATTCGAGAAG TAGAAGCAAT GATTAAGGAA ATTAAGAAAG AGTADGGGCA TATNCAAGCT
 TTGCTGGTTA CTGGGCATTT AGGCGTAGAT GAAAGCAAT GCGATATATG GGTGCTGAT
 ACGCTAGCAG AAACCCCTTA TCAAAACATAT CCTGAGTATG ATATGATCTT GATTGATGGA
 CATTCCGATA CAGCCGCTCA AAGTGGCAAA CGTTATATTA AAGTATAT TAATGCAACA
 GGTAAATTAT TAAATAATGT TGCGATCGTC ACAGCAATTA AGATGATGCG AATTAAGAAA
 ACAACAAAAT TGATTTCAAG AGCAGAGCTG CTAGATATCT TACAAAAGCT GGTAGTTAAA
 GCCATCGTTG ATGAAGCAGG TACGAATTTT AAAGCTGAAA ATGAAAAGCT AATTTCTGAT
 TATATTCCAT TCACATTGCA TGGACAACGA TATGCGCAAG AGGCTTTTGA CCAACCTGCT
 GGAATTTTGA TTGCTGATGC GATTATGTCA TATGCGCAAG AGGCTTTTGA CCAACCTGCT
 GATTTTGCAG TAACTAATGG TGCGCGCATT CGGCTGATTA TTAACAAAG GGTAAATTAAA
 GTTGGGGATG TCATTGCTGT GTTACCTTTT GGTAAATATG TTGCGCAAT TGAAGTAACC
 GGCGCCCAAG TTAAAGAAAT GTTTGAAATG TGTGTTCTCT GATTTCTCA AAAAGATGAG
 AATGGCAGAA TTTTACTAGA TGATGCTGCG CAGCGCAAT TCGCGCAAA TGTGCTTTC
 CTACATGTTT CAAGCTCCAT TCGTATCCAC TATGATGCTG TAAAGCTG TACTGCTTG
 GCTAGTGAGC AAGGCAATGA AACAGGACAA AGGATTTCTG TATGCTGCTT ATTAGGAATA
 GAAATTAAAA ATCGGCAAAAC ACAAAGGTTT GAAGCAATGA ATGAGAAAGC ACAAATCCGG
 ATGGCTACCA ATGATTTCTT AGCTGCTGCT TATGATGCTG TAAAGCTG TACTGCTTG
 CGAGAAGAAG GCATTTCACT AGATTCTGTC TTAATTGATG AATTGAAGAG TGTAAACCAGC
 TTGCGGTTGT ATCGTGACAG AACGACGATT GATTTATGAT AATATAAGCA ATCATTTCCA
 GGCGAACGAA TTGTTCTAT TTGGAAGAA GCTTACAAAG AATTAATGCG TGTAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACCCG AAACCAACAG CAGAAATGCG ATAGCAACC
 AATAAACAAA ACCAAGCGGG AGCAAGACAG AGCAATGCTG CGGTAACAGA GAAGAAAAAG
 TATGGCGGCT TTTTACCTAA AACGGGTACA GAAACAGAAA CGCTTCTGCT ATATGGTTTA
 CTGTTCTGTT GACTTTCTTC TTCTGGCTGG TATATTATTA AAGAGCTAA CAAAGCTAGT
 TAG

EF121-2 (SEQ ID NO:450)

VKKL SFKKVKWGMH FLMAVALIAP SVTSTAYAVE TTHLSSHAV TSTTDSSREQ
 EPVITQETTD IKQEAPNQAT SLSVKQSQET TATTTETTHL TSAEKERTS TPQKITILGT
 SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVRAQNPALV VLDNGSTMIQ GTILTDLLYN
 KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLFLIPL TQCATPHIL SANTYKNEDG
 LRFVEGTTHK ELDFNQDGGP DLKVGIIIGLT IPRIPKXGSI RVTSLSNPLPL KEEAEKAVTE
 LKANDQADII VASIHAGQQN SDPAASADQV IENVAGIDAL ILGHDHLGPT KQDAAPNGKT
 VPVGPGKDTG TEVVKIILSV AKNADKWEVQ EGTATINPTT NPADAEAKA ATKEYHEKTR
 AFIQEEIGTA TADFLPFQEI FGIPFAQLQP TAMISLIIIN QFEVTGAPLS AALFKYDSK
 LPAGKISYAT IFDIYKYPNT LVSVPINGEN LLNYLEKQSA YNNQTQFQDL TISFNPINRV
 YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPNSPAKENT IANNVYRGG LRSQGIQVGE

TABLE 1. Nucleotide and Amino Acid Sequences of *H. faecalis* Genes.

PIKNSDPETL RGMIVDYIKK KGTLDPEQEI ERNMSLISGM FDEKWRKAI EIMVNDGTLQI
 PTSPDGRTPN AAAITKQDVR NAGFDLDNAY TIMHTTTHHG RLEAGKGELG MARLKTFKDQ
 ENPTLMVDAG DVFQGLPISN FSKGADMAKA MNEVGYTAMA VGNHEFDGGL EIALGYKDQL
 NFPISSNTY YKDGSGRVFD PYTIVEKSGK KFAIMGVTTD ETATKTHPKN VEVWTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIVFQST LAETLSQTVF ELDITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEFTTFT TRLISAEELL ELPEHPAVKA
 IVDEARTNFN AENEKVIVDY IPFTLDGQRE NVETRETNLR INIGDALMSY GSDAFSQPAD
 FAVTNGGGIR ADIKQGGPIKV GDVIAVLPPG NSTAQIQVTS AQVKEMFEMS VRSIPQKDEN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPCETLA SDEGNETGQT IMSSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMIGSER EEGISLDSVL IEYLKSATSL
 RLYRAATTID LAQYKEPFPG ERIVSISEEA YKELJCGSET PHDPKPKDPH PTPETPVATN
 KQNQAGARQS NPSVTEKKKY GGFLPKTGT EETLAINGLL FVGLSSSSUY IYPRNKAS

EF121-3 (SEQ ID NO:451)

ACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATTG AAGTAGAAAA
 CAAGAACCAG TCATTACACA GGAAACAACA GATATGAAAG AAGAGGAGG AANTCAGGCT
 ACGAGTGACA GTGTCAAGCA GTCACAAGAA AGCAGAGGAG CAACAGAGAG GAGGAATTTA
 GAAACGTCAG TCGCTGAAAA AGAAGAAACG AGGAGGAGG AAAAAATAGG AMTTTATAGT
 ACGTCAGATG TTCATGGTCA ATTATGGAAT TGCTCTTATG AAGATGATAA AGAAGTACCA
 GTTGGTTTTGT CCCAAGTAAG TACAGTCGTT AAGCAGAGG GGGCAGAAAA CCGAGCAGGC
 ACCGTTTTTAA TTGATAATGG CGACAATATT CAAGGAGGTA TTTTAAAGAA TGACTTGTAT
 AATAAAGCGC CTTTGTAGTAA TGAAAAGACC CATGAGAGTA TGAGGAGGAT GAATGTGATG
 AAGTATGATG CAATGGTTTT GGGAAATCAT GATTTTATTT TTCTTTTATG GTTAATCAAAA
 AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTCTCTTATG ATAGCTACAA TAAGGAAGAT
 GGTCTTCGTT TTGTTGAAGG GACTACCACG AAGAGAGGTA ATTTTATTTA AGATGGGCAG
 CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTTTAT AGATTTCTTT GTGGGATGGC
 CCTCGTGTTA CTTGCTTAA TTTTTTACCT TTGAGAGGAG AAGAGAGGAA AGGAGTTACT
 GAGTTGAAAG CTAACGATCA GGCTGACATT ATTTTCTTCT CGATTTCATG GGGACAACAA
 AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATCTGCGGCG GATTGATGCG
 TATATTCTGG GTCATGACCA CCTTTCTTTT ACAGAGGAG GAGGAGGAGT GAATGAGAAA
 ACTGTACCGG TAGGGGGACC GAAAGATACG GGGAGAGGAG TTCTGAGGAT TGATCTTTCA
 GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAGGATA CAGCAAGGAT TGTACCAACA
 ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGGAGGAA AAGAAATGCA TGAAAAAACG
 CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAAGAGGAG ATTTTCTTCT AAAACAAGAA
 ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAAGAGGAG TGATTTCTTT AATTAATAAC
 GTTCAAAAAA AAGTAACGGG CGCACAATTA AGTGGGAGAG CGCTGTTTAA ATACGACAGT
 AAATTACCTG CGGGGAAGAT TTCCTATGCC ACATTTTCTG ATATCTATCA ATACCCGAAT
 ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AATTATCTGA AGTATTTAGA AAAACAAGGG
 GCGTACTATA ACCAAACACA GCCAGATGAT TTGAGGATTA GTTTTATCTG AACATTTCGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GACTAGAGGA TTAGATTTCT AAAACAGAGT
 GGTGAACGAA TTGTAGATGC GAAAATTGAC GGTCAAGGAG TTAGATCTCT CAAAGAAATAT
 ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGGTA GCGAAGGAGT TGAAGTAGGG
 GAACCTATTA AAAATTCTGA TCCAGAAACC TTGAGAGGAA TTAGTTGTTA TTATATTAAG
 AAAAAAGGAA CTCTTGATCC AGAACAAGAA ATGAGAGGAA ATGAGTCAAT TATTGGGACA
 AATTTTGATG AAAAAATGGG TGCCAAAGCA ATGAAATTAG TGAATGAGCG CACTCTTCAA
 ATTCCGACTT CTCCTGATGG ACGTACACCA AAGGCGG

EF121-4 (SEQ ID NO:452)

QSSEAV TSTTDSSRKQ

EPVITQETTD IKQEPNQAT SDSVKQSQET TATTEFTTLE TSAEKEEIS TPQKITILGT
 SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVLAQHFAET VLIDNSDNIQ GTILDDLYN

TABLE 1. Nucleotide and Amino Acid Sequence of the *hmd* Genes.

KAPLVNEKTH	PMITAMNMMK	YDAMCLGNFE	FNKSLN	QV	VEATHYIL	SMITYNKEDG
LRFVEGTTTTK	ELDFNQDGGP	DLKUSIISLT	IFHIFN	QV	FTISLNFLML	PLAEKAVTE
LKANDQADII	VASIHAGQON	SEPAASADQV	ILHFM	QV	ILHFM	PLSAAPNGKT
VPVGGPKDTG	TEVTKIDLSV	AKNADKWEHQ	EGATIN	QV	NTNADENYKA	ATHEYHEKTR
APIQEEIGTA	TADFLPKQEI	KSLPENLQFP	TAHIVH	QV	THNTGATLS	AAALFKYDSK
LPAGKISYAT	IFDIYKYPNT	LNSVPINGFN	LIFVH	QV	THNTGATLS	TGDFNPNIHV
YNYDMISGVD	YKIDISKPMG	ERINDAKNDG	QPLI	QV	INNTNYFQD	LASQGIQVGE
PIKNSDPETL	RSMINDYIKK	KSTADPEEI	EREND	QV	THNTGATLS	ELVNDSTLQI
PTSPDGRTPN	A					

EF122-1 (SEQ ID NO:453)

TGAAACACAA	GSAGSAAATF	TGTGAAAAAG	TTAGATTA	AAAAASTDAA	GTGGGSCATG
CATTTTTTAA	TGCTGTTC	GTTGATAGCG	CGAATTA	CTAGTACGCT	ATAGGAGTA
GAAACAACGA	GTCACAAAG	TTCAGAAAG	GTAAATTA	CTAGGAGTTC	AGTAGAAAA
CAAGAACCAG	TCATTACADA	GGAAACAANA	CAATTA	ATAGGAGTTC	AAATCAGGCT
ACGAGTGACA	GTCTAAGDA	GTCACAAAG	AGATTA	CTAGGAGTTC	CAAGGAATTTA
GAAACGTCOA	TCCTGAAAA	AGAAGAAAG	AGGAGTTC	AAAAAATAC	ATTTTTAGGT
ACGTCAGATG	TTTATGGTCA	ATTATGGAAT	TGCTTA	AAATATGATA	AGAACTACCA
GTTGGTTTGT	CCCAAGTAA3	TACAGTCTTT	AAAGATTA	CTAGGAGTTC	CCGAGCAGGC
ACCGTTTTAA	TTGATAAT33	CGACAATATT	CAAGGATTA	TTTAAATGA	TGATTTGTAT
AATAAAGCGC	CTTTAGTGAA	TGAAAAAGAC	CATGAA	TTAGGAGTTC	GAATGTGATG
AAGTATGATG	CAAT3GTTTT	GGSAAATCAT	GATTTTAT	TTGCTTAC	GTTAATCAAA
AAAATTCAAC	AAGAAGCCAC	TTTTGCAATC	TTTCTTA	ATAGGAGTTC	TAAGGAAGAT
GGTCTTCGTT	TTGTTGAAG3	GACTAGCAGC	AAAGGATTC	ATTTTAATCA	AGATGGGCAG
CCAGATTTAA	AAGTTGGGAT	TATGCTTCA	AGATTTCT	AGATTTCTTT	GTGGGATGGC
CCTCGTGTTA	CTTCGCTTAA	TTTTTTACCT	TTGAAAGAG	AAAGGAGTTC	AGGATTTACT
GAGTTGAAAG	CTAACGATCA	GGTGAATTT	ATTCTTCT	CTATTCATCC	CCGACAACAA
AATAGTGATC	CGGCTGCCAG	TGCCGAGCA	GTAATTTCT	AGGAGTTC	GAATGTGATG
TATATTCTGG	CTCATGACCA	CGTTCTTTT	ACCAAGGAG	GAAGGAGTTC	GAATGGAAAA
ACTGTACCGG	TAGGGGACCC	GAAAGATAG	GGACAGTTC	TTGAGGATTC	TGATTTTCA
GTTGCTAAAA	ATGCCGATAA	GTGGGAAAT3	CAAGGATTC	GAAGGAGTTC	TGTACCAACA
ACGAATGTTT	CAGCAGATGA	AGCAATTAAG	GTAGGAGTTC	AAAGGATTC	TGAAAAAACC
CGAGCGTTTA	TTCAGGAGGA	GATGAGGACA	GAAGGATTC	ATTTTCTTAC	AAAAACAAGAA
ATTAAAGGAA	TTCCCGAAGC	ACAATTAACA	CCAAGGATTC	TGATTTCTTT	AATTAATAAC
GTTCAAAAAG	AAGTAACGGG	CGCACAATTA	AGTGGGAGC	CGCTGTTTAA	ATAGGACAGT
AAATTACCTG	CGGGGAAGAT	TTCTAT333	AGGATTTT	ATATCTACAA	ATAGCCGAAT
ACCTTAGTGA	GTGTTCCCAT	TAACGGTGAA	AACTTAGTGA	AGTATTTAGA	AAAAACAAGG
GCGTACTATA	ACCAACACA	GCCGATGAT	TTAGGATTC	TTTAAATTC	AAACATTCGT
GTATATAACT	ATGACATGAT	TTCTGGAGTG	GATTAACA	TTGACATTT	AAAGCCAGTG
GGTGAACGAA	TTGTAGAT3C	GAAAATT3AC	GGTAAATTC	TTGATCTTTC	CAAGGAATAT
ACGATTGCTA	TGAATAATTA	TCGTTAG33C	GGTTTATTA	GAAGGAGTTC	TGAAGTAGGG
GAACCTATTA	AAAATTCTGA	TCCAGAAACC	TTAGGAGTTC	TTATTTGTTA	TTATATTAAAG
AAAAAAGGAA	CTCTTGATCC	AGAACAAGAA	ATGAAATTC	ATGAGTTCAT	TATTTGGGACA
AATTTTGATG	AAAAATGGCG	TGCCAAAGCA	ATGAAATTC	TTAATGAGCG	CACTCTTCAA
ATTCCGACTT	CTCTTGATGG	ACGTACAGCA	AAAGGAGTTC	CTATTAGGAA	AGAGATGTCT
CGTAATGCGG	GCTTTGATTT	AGATAATGCA	TATAGGATTC	TTGACAGAAA	TGACCTTCAT
GGCCGACTAG	AAGCAGGGA	AGGCGAATTA	GCTATGAGTTC	GTGAAAGAA	CTTTAAAGAC
CAAGAAAACC	CAACCTTGAT	GGTGGATGCA	GGGATGTTT	TTGAAAGGAT	AGCAATCTCC
AATTTCTCCA	AAGGCGCGGA	TATGGCCAAA	GCAATGAGTTC	AASTTGGTTA	TGAT3CCATG
GCGGTGGGAA	ATCACGAGTT	TGATTTT33T	TTAGAGATTC	CACTAGGTTA	TAAAGACCAA
CTGAATTTTC	CGATTTTATC	TAGTAATAAG	TATAGAGTTC	ATGGGAGTTC	AAAGGTTTTT
GATCCGTATA	CAATCGTAGA	AAAATCGG33	AAAGGATTC	CACTCTTAGG	TGTGACGACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAAA ABGTGACATT TAAAGACCCG
 ATTCCAGAAG TAGAAGCAGT GATTAAGSAA ATTAAGSAGA AATACGJGGA TATNCAAGCT
 TTCGTGGTTA CTGGGCATTT AGGCGTASAT GAAACGABBC CECATATCTG GCGTGGTGAT
 ACGCTAGCAG AAACCCCTTAG TCAAACATAT CCGTACIAG AATCACTGT GATTGATGGA
 CATTGCGATA CAGCCGTCGA AAGTGGCAAA CGTTATBACA ABGTBATCTA TCTCAAAACA
 GGTAATTATT TAAATAATGT TGGGATCSTC ATAGCIBAG ABAGTGAACC AACTAAGAAA
 ACAACAAAAT TGATTTACAG AGCAGAGCTG CTAGAATTAG CAGAAAACCC GGCAGTAAAA
 GCCATCGTTG ATGAAGCACG TACGAATTTT AACGCTBAAA ATGAAAAAST AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATBTGC GACACACAGA GACCAACTTA
 GGGAAATTTGA TTGGTGATGC GATTATGTCA TATBGCIAAG ABGCTTTAG GGAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CCBCTBATA TTAACACAGG GCAATTAATA
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 CTACATGTTT CAAGCTCCAT TCGTATCAC TATBATTCCA CAAAACJABG TACTCGCTTG
 GCTAGTGACG AAGGCAATGA AACAGGACAA ACBATTBTGC CTAGTGBOST ATTAGGAATA
 GAAATTAATA ATCGGCAAAC ACAAAGTTT GAACCAITBG ATGABAAGAA ABAATACCGG
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 CGAGAAGAAG GGATTTCACT AGATTCTBCT TTAATTBAAE ATTTGAAAAG TSCAACCAGC
 TTGCGGTTGT ATCGTGACG AACGACGATT GATTTAGAC AATATAAGA ACCATTCCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAASAA GCTTACAAAB ATTIAAFCGB TCGAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACBGC AAACCAABAC TAAAAAACCC ABTAGCAACC
 AATAAACAAA ACCAAGCGGG AGCAAGACAG ASCAATBBAE TCGTAACAGA CAAGAAAAAG
 TATGGCGGCT TTTTACCTAA AACGGGTACA GAAACABAAA TCGTTGATTE ABATGGTTTA
 CTGTTCTGTTG GACTTCTTTC TTCTGGCTGG TATATTITATA AACGACBIAA CAAAGCTAGT
 TAG

EF122-2 (SEQ ID NO:454)

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 EPVITQETTD IKQEAPNQAT SDSVKQSQET TATTTETMLE TSLAEKEETS TPQKITILGT
 SDVHGQLWNW SYEDDKELPV GLSQVSTVNV QVRAQNPAST VLIDNGDNIQ GTILTDDLYN
 KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLHLEKK TQCEATFPIL SANTYNKEDG
 LRFVEGTTTK ELDFNQDQGP DLKVGIIGLT IPHIPWDDP FVTSLNFLPL HEEAEKAVTE
 LKANDQADII VASIHAGQON SDPAASADQV IENVASIDAY ILGHDHLSFT KQGAAPNGKT
 VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATVETTT IUPALEAVKA ATKEYHEKTR
 AFIQEEIGTA TADFLPKQEI KGIPEAQLQP TANISIDHNV QKEVTGAQLS AAALFKYDSK
 LPAGKISYAT IFDIYKYPNT LVSVPINGEN ILHYLEKQGA VYNQTKPDDL TTSFNPNIHV
 YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPLDPAREYT IANTNYRYGG LASQGIQVGE
 PIKNSDPETL RGMIVDIYKK KGTLDPEQEI ERNWSLIGTN FDEKWFAKAI ELVNDGTLQI
 PTSPDGRTPN AAAITKQDVR NAGFDLDNAY TIMHTHEDHG RLEAGFGELG MARLKTFKDQ
 ENPTLMVDAG DVFQGLPISN FSKGADMAKA MNEVGYDAMA VGNHEFDGFL EIALGYKDQL
 NFPILSSNTY YKDGSGRVFD PYTIVEKSGK KFAIVGVVTP ETATKTHPPN VEKVTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIVRDET LAETLSQTYP ELDTITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APSEPTTET TFLISAAELL ELFENPAVKA
 IVDEARTNFN AENEKIVIDY IPFTLDGQRE NVETRETHLG HLIGDAIMSY GGTAFSQPAD
 FAVTNGGGIR ADIKQGPIKV GDVIAVLPPG NSIAQLQVTE AAVKHEMFEMS VESIPQKDEN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKFBTHLA SDEGNHTGQT LUGSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMQGER BEGISLDSVL IEYLKSATSL
 RLYRAATTID LAQYKEPFPG ERIVSISEEA YKELIGGRET PNPDPKPDPK PTPETPVATN
 KQNQAGARQS NPSVTEKKKY GGFLPKTGT TETDAILYGLL FVGLSSSGWY IYFRNKAS

EF122-3 (SEQ ID NO:455)

TABLE 1. Nucleotide and Amino Acid Sequence of *Escherichia coli* Genes

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 ATTCCGACTT CTGCTGATGG AGGTACATCA AAGGATTC GATTACGAA / AAGATGTC
 CGTAATGGGG GCTTTGATTT AGATAATGCA TACAGCAAAA TACAGCAAAA TACGCTTCAT
 GGCCGACTAG AAGCAGGGAA AGGCGAATTA GGTATCTT GCTTAAAAAT TTCTAAAGAC
 CAGGAAAAAC CAACCTTGAT GGTGATGCA GAGATTCCT TCAAGGATT AACAATCTCC
 AATTTCTCCA AAGGCGCGCA TATGCGCAAA GCAATGATTA AATTGCTTA TATGCGCATG
 GCGGTGGGAA ATGAGGAGTT TGATTTTGGT TTGAGGATTA TATGAGTTA TGAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATACG TACTAGAAA ATGAGAGTGG AAGGCTTTTT
 GATCCGTATA CAATCTAGCA AAAATCTGCG AAAAAGCTTC CATTGTAAG TATGAGGACC
 CCAGAAACAG CAACGAAAAC ACACCGGAAA AAGTATGCA AAGTACATTA TGAAGACCCG
 ATTCCAGAA TAGAAGCAAT GATTAAGGAA ATTAAGGAAA AATAGCGGA TATTCAGCT
 TTCTGGGTTA CTGCGCATTT AGGCTAGAT GAAAGCAAG CCGATATCTG GAGTGGTGAT
 ACCGTAGCAG AAACCGTTAG TCAAGCATAT CCGTAGTAA AGATCACTCT CATTGATGGA
 CATTCGCATA CAGGCTCGA AAGTGGCAAA CGTTATCA AAGTATCTA TCTCAAAACA
 GGTAAATTAT TAAATAATGT TGGGATGCTC ACAGCAGTAC AAGTGAAGC AACTAAGAAA
 ACAACAAAAT TGATTTGAGC AGCAGAGCTG CTAGATTTG CAGAAAACAG CAGAGTTAAA
 GCCATCTGTC ATGAAGCAGC TACGAATTTT AAGCTTGAAG ACAGAAAAGT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAAAGA GAAATGTAAG CACAGAGCA GAGTAACCTTA
 GGGAAATTGA TTGGTGATGC GATTATGCTA TATGCGCAAG AAGGCTTTAG CAACTGCT
 GATTTTGCA TAACATAATG TGGCGGATTT CGCGCTGAAA TGAAGCAAG CAAATTAATA
 GTTGGGATG TCATTGCTGT GTTACCTTTT GCGAATAGT TGGGCAAT TGAAGTAACC
 GGCGCCCAA TTAAGGAAAT GTTTGAAATG TCTGTTTCT CATTGCAAG AAGAGATGAG
 AATGGCACAA TTTTACTAGA TGATGCTGTC CAACCAAAAG TGGGCGCAAA TATGCTTTTC
 CTACATGTTT CAAGCTCCAT TCGTATGCTC TATGATTTCA CAAAAGCAGC TACTGCTTG
 GCTAGTGAGC AAGGCAATGA AACAGGACAA AGGATTTGAG GTAGTGGCTT AATAGGAATA
 GAAATTAATA ATCGGCAAA ACAGAAATTT GAACCATGAG ATGAGAGAGAA AAGATACCGG
 ATGGCTACCA ATGATTTCTT AGCTGCTGCT GGTGATGCTT AGCATATGCT AAGTGGTGAA
 CGAGAAGAAG GGATTTCACT AGATTCTGCT TTAATGGAAT GTTGAAGAA TGAAGCAGC
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 GGCGAACGAA TTGTTTCTAT TTCGGAGGAA GCTTACAGAG AGTAAATCTG TGAAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACCGG AAACCAAAAG CAGAAACAGT AATAGCAACC
 AATAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCTAT CCGTAACAGA CAGAGAAAAG
 TATGGCGGCT TT

EF122-4 (SEQ ID NO:456)

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 NFPILSSNTY YKLGSGRVFD PYTIVEKSGK KFAIVGNVTH EATKTHPKN VEKVTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIWAGCT LAETLSQTYF EMBETVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTTET TRLISAAELL ELFENPAVKA
 IVDEARTNFN AENEKIVVDY IPFTLDGQRE NVETRETHNG INFGDAIMSY GWDAPSQPAD
 FAVTNGGGIR ADIKQGPVKV GDVIAVLPPF NSIAQIQITG ATTKEMFEMS VHSIPQKDEN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPGTKLA SDEGNETGQT IYDSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMLGGER EESISLDSVL IETLKSATSL
 RLYRAATTID LAQYKEPFPF ERIVSISEBA YKELIGGSET PHFDPKPDPE PEPETPVATN
 KQNQAGARQS NPSVTEKKKY GGF

EF123-1 (SEQ ID NO:457)

TAAAATAAAA AATTGGTACG AAGTGAACGT TCTCTCTAT GTCTCGTTAG TAGAGGAAGG
 ATGAAAGAAA TGAGAAAGAA TGGTCCAAIG GTAAACCGTT GCTCTACGG GTTGATGTGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTGTTACTTG	TTCTAAATTA	TGGCACACA	CTCATGGCTT	TGGGCGAAGA	GGTTAACAGC
GATGGCCAGT	TAACGTTAGG	AGAAGTGAAG	CAAACCAGCC	AGAAAGAAAT	GACCTTAGCG
CTTCAAGGAA	AAGCACAACC	AGTAACACAA	GAGGTTGTAG	TGCATTATAG	TGCCAATGTG
TCAATCAAAG	CTGCACATTG	GGCAGCGCTC	AATAATACGG	GCAAGATTCA	AGTGGATGAC
CAGAAGAAAC	AGATTCAAAT	TGAATTGAAT	CAGCAAGCGT	TAGCAGATAC	GTTAGTCTTA
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TTGACGTTAA	AGACTGGTAC	TGATCCGACA	GAATCAACGG	CANTACCGAG	TGCGCCAGCC
GCATCAGCGA	ATGAAGGTTT	AACAGAAAGAA	GCATCTACAA	ACTGCTCTGT	TGCTCGTTCC
TCCGAAGAAA	CTGTCGCCAG	CACGACAAAA	GCGATAGAAA	GTAAACAAC	TGAATCGACG
ACTGTCAAAC	CGCGCGTAGC	AGGACCAACA	GATATCAGTG	ATTATTTTAC	AGGTGATGAA
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GATGTGCGAG	AACAAATGAA	AGCAGGCGAT	TACTTCGAGT	TTCAATTACC	TGCGCAATTTG
AAACCTAATA	AACCAAGTTC	AGGTGATTTA	GTTGATGCAG	AAGGCAATCT	CTATGGAACC
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AGTGACATTC	ACGGGGACTT	TTCTTTAGAT	ACTCATTGTA	ATGATTCAGA	TGGCGGGGGC
CCAGGAGATT	GGGTGATTGA	TATTCCTACA	CAAGAAGATT	TGCGCCTGT	ATGATTCCTA
ATTGTCCCAG	ATACCGAACA	ACAAATTGAT	AAACAAGGCT	ATTTTATATC	AACGCCCAAT
CCTAGTGCGA	TTACTTGGAC	GGTAGATATC	AATCAAGCGA	TGAAGATCA	AACAAATCCA
ACTGTGACGG	AAACATGGCC	AACAGGGAAT	ACCTTTAAGT	CGTGAAGAT	CTATGAGTTA
GTGATGAATC	TTGATGGAAC	AATTAAAGAA	GTGGGTGCGG	AATTTAGTCC	AGATGAATAT
ACCGTTGATA	AAAATGGCAA	TGTGACGATT	AAAGGTGACA	CGAACAAAGC	GTATCGTCTT
GAGTAGCAAA	CGACGATTGA	CGAGGCGGTT	ATTCCAGATG	GGGCGCGCGA	TGIGCCTTTT
AAAAATCACG	CGACGTTAAT	AAGTGATAAT	AATCCAAATG	CGTTATATGC	TGAAGCAACT
GTTACCGCCA	CATATGGCAA	AATGTTATAC	AAGCGCAATA	TATATTCAGA	CGAAGCCAAT
CAAGAATTCA	CTTGGGAAAT	TAATACAAAC	TATGGTGAAAT	AAACCATTCG	AAAAGACCAA
GCAGTCATTA	CAGACACAAT	GGGGGATAAT	TTAACGTTTG	AAACAATATC	TTTACATTTA
TATTCAGTGA	CATTTGATGA	CAAAGGAAAT	GAAGTCGTTG	GAGCAGAACT	TTTGAAGGA
AAAGATTACA	AAGTGGTAAT	CAACGGAGAC	GGTTCCTTTT	CAATTSACTT	TTTACATGAT
GTGACTGGCG	CAGTCAAGAT	TGATTATAAA	ACCAAGTTTG	ATGGAATTGT	CGAAGGCGAT
GTTGCGGTGA	ATAATCGTGT	GGATGTTGCG	ACTGGTCAGC	ATTGAGAAAG	TGATGGCACA
GCCAGTCAAC	AAAATATTAT	TAAAAACACT	GGTGCAGTTG	ATTATCAAAA	TGCAACGATT
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CAAGGTCTTT	CACGTGATGT	GACAGGAAAA	GTTTCTATTG	AACATGGTGG	CGAATCAGTG
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GTGCTAGATC	CCGAGTCATT	GGTGATTTAC	GGTACCAACG	TAAACAGAAGA	CGGAATATT
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GATAATGAAA	CAGGACAACA	AAAAATGCTC	GTTAAAATG	CGATATTTGA	AGCACCTTAT
TATATGGAAT	ATCGTAGTTT	AGTGACTTCT	TCAGCGGCGG	GGAATACAGA	CACGGTATCC
AACCAAGTGT	CAATTACTGG	AAATGTTTCA	GAAGTCGTTG	ATGAGGATGA	CAATGGCGAT
GTGGTCGTTG	ACATTGATCA	CAGTGGCGGG	CATGCCACAG	GGAATAAAGG	CAAAATTCAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ACAGTTTGGG ACCAATTAGT TAAAGGCGGA CTCATTACTA TTGATGAAGA AATTTCAGCC
BAAGGAGGAC AACCAACCAT TATTAAAAAC GATCTTAATA AACTATTTTT AAAAAAATG
GATGAGAAGG GTAAAAAGTT AGTCAATGCT CTTTAAANT TAAATATGCT CAAACACG
CCGTTTACTG ATTGGGAAGA AATTGCGCTT CCGCCGATC GAATTAACCG GATGGCCAG
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ATTGCTGATG TTCATCTCAA AATGCTTAAT TACCAAGGTT CTGCTGAAGT AATTAAAAAA
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CCAGGAAAAAT ATCAATTTGT GBAACCAAAA GCGGAGGAG GGTATTTTTT AAGACTGAA
CCAAGTGGTT TCACGATTGT AGCAAGGAT GCGGCAAAAC CAGCAACAGT TATACCAAG
GCTAAGTTT TTAAGTATCA AGGCAAGGCT AATTTAATCA AAAAAATGT GATGACAC
TTATTAAGTG GTGGACATT TAAAGTCTTT GATGCAAGG CAGAAAGAT TAAAGAGGC
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TTTGTAGAAA CCAAGCGGT AACAGGCTAT TTACTTAAATA CAGGCGGAT CTTATTTGAA
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GATGGCAAAA TTATCTTTAG AGACTTGGGG CAGGTAAGCT ATTATTAACA AAAAAACAA
GCACCAAAAT TACCAGATG GCGAGATTAT ATATTTTATC CTATTTAGT AAAAAATGAA
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AAAGGACGCG CCGTCTTTAA GAAATTTGAT GCAATGCGA ACCAGTTCT AATGAGATT
TTTAAATTGT ATCGAATGSA AAACGGGAA AAAATTTTTG AAGGAGAGT AATGCTGAA
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GCCGATCAGC AGAATCAGGC CCAAGGTTCA GAGATAAGAT TTTTAAATG TTAGGAGAA
AAAGTTTCTG AAATAACAAC GGATAAGAT GGTAAATTT AGGTAAAGG GTTAAATGAA
GGGCATTACG TTTTAGTGSA AACGAAAGCA CCAAGGCT ATTTGTTAGA CAAAGCGTA
CATCCATTG ATGTAACCG CCAATTAGGA AAGAGCAGC CAATGCTTT AGGCTATCTT
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GGTGGCGGT TTAAGGTCAT TGATGAAACA GGGCAACCG TAGATGAGCA AATCAATCTG
ATGTCTGACA AGCAAGGCAA AGTCATTGCG AAAACTTAG CACCGGGAAC GATGCTTTT
GTGGAGACAC AAGCGCCAAC TAGCTATCTT CTTAATGAAA GAGCAAGCGC AAGCTTTACG
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TACCAAGGTG CTGCCAAGST GGTGAAATTT GATCAGCAAA AGAATGCTT AATGCTGCT
GAATTTAAAG TGACAGATGC AGAGACAGG CAAACTGTG CTGTTTCAAT AATTTCTGAC
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CGGAAAGACA AACCTGAAGT CGTGAATGG GGCAGCTTTG TTAAGGAGAA AATGCTGTA
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EF123-2 (SEQ ID NO:458)

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KKQIQIELNQ QALADTLVLT LNPTATEDVT FSYBQQQRAL TLKGTDPTE STATSSPAA
SANEGSTEEA STNSSVPRSS EETVASTTKA IESKTTSTT VKRWAGPTD IATFTGDET

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GDWVIDIPTQ EDLPPVVIPI VPDTEQQIDK QGHFDFTPNP SALTWTVDIN QAMFLQTNPT
 VTETWPTGNT FKSVMVYELV MNLDGTIKEV GPFLSIDEYT VDFKGNVTIF GDTTKAYRLE
 YQTTIDEAVI PDGGGDVPFK NHATLTSNN PHLDAEATV TATYCHMLLF FHLIDYDEANQ
 EFTWEINYNY GEQTIPKQQA VITDTMGDNL TFEPDLSHLY SVTFDEKGNF VMSAELVEGK
 DYKVVINGDG SFAIDFLHDV TGAVKIDYKT FVDGIVEGDV AVNHVVDVGT GCHSEDDGTA
 SQQNIKNTG AVDYQNSTIG WTLAVNQNNY IMENAVITDT YEPVFGLTMY FHLAVVKDIT
 TGAQLTLGKD FMVEITRNAD GETGFEVSFI GAYAKTSDAF HITYTTFFDM TELLANNPAL
 DHYRNTAAID WTDEAGNNHH SEDSKPFKPL PAFDLNAQKS CVTHAVTKEI TETIAVHLSN
 NRLVDAFLTD PILTNQTYLA GSKLVYEGNT KPDGSVEKVK PTQPLEDITM EEPSEKNQNT
 WRVDFPNDSR TYVIEFKTSV DEKVIKESAS YDNTASYTNQ GSSPFWTGKV SIQGGGESVK
 KGGEYHKDDP DHVYWHVMIN GAQSVLDDVV ICHTFSPNQV LDPEFLVIYC THVTDGTTIT
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EF123-3 (SEQ ID NO:459)

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TABLE 1. Nucleotide and Ammo Acid Sequences of *E. faecalis* Genes.

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EF123-4 (SEQ ID NO:460)

EEVNSD

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EF124-1 (SEQ ID NO:461)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TABLE 1. Nucleotide and Ammo Acid Sequences of *E. faecalis* Genes.

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EF124-2 (SEQ ID NO:462)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EF124-3 (SEQ ID NO:463)

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EF124-4 (SEQ ID NO:464)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

AF HITYTTFFDV TELDANNPAL

DHYRNTAAID	WDEAGNNHH	SEIHHFPHFL	PANLHMHKS	GYNHNTYFI	TEANNLSN
NRLVDAFLTD	PILTNQTYLA	GSNHYEGNT	KPSCNHHVK	PTPLTDTIM	TEPHKNQNT
WRVDFPNDSR	TYVIBFKTSV	DEHVEGSAE	YDNTAHTNQ	GSNHYTSGN	TEPHGESVK
KGSEYHKDDP	DHVMHVMIN	GATVULSDIV	ITVHMHNV	LDPEELVIYG	TEPHEDGTIT
PDKSVILEEG	HDYTLVTTD	NETSQQKIV	KMARLAPFY	MEHRELVTSS	TEPHDTVSN
QVSITGNGSE	VHGDENGDV	VVDITHSSGH	ALSHSHIQL	KHFMDETTI	TEPHANFQIWD
QAKTQVLREG	TVDATGVITF	BSMTHQYIL	VEHMTSGYT	VSEELAKGRV	TEPHETSAAE
GAQPTTIKND	VNKVFLEKMD	ENHFKLNAR	FKLEHMTTP	FTWEEVPLA	TEPHANGQL
EVDSLKPGLY	QFTEIEAPTG	KLSDTIPKRF	IVPTNAGQI	RDHMKMLNY	TEPHALIKKD
QAGNPLAGAE	FSVLDTTGQA	VREHLVSDAN	GKVTHTLAP	GHTVPEVTKA	TEPHVLLNTEP
SAFTIAASDR	GKPATVIATA	NFNHYGPAK	LIHHHNGHL	LSGATFKVLD	TEPHHTIQTGL
TTNNQG					

EF125-1 (SEQ ID NO:465)

TAAAAATAAAA	AATTGGTAGG	AAGTGAAGGT	TCTGCTAT	GTTCGGTTAG	CAAGGAAGG
ATGAAAGAAA	TGAGAAAGAA	TGCTCAATG	GTAAAGCTT	GGTCTACGG	CTGATGTGT
TTGTTACTTG	TTCTAAATTA	TGACACACCA	CTAAAGCTT	TGAGGAAGA	CTTAACAGC
GATGGCCAGT	TAACGTTAGG	AGAACTGAAG	CAAGCAGCC	AGAAAGAAAT	CTGCTTAGCG
CTTCAAGGAA	AAGCACAACC	AGTAATACAA	GAGGCTTAG	TGATTTATAG	CTGCTATGTG
TCAATCAAAAG	CTGCACATTG	GGCAGCGCC	AATGATAGG	GCAGATTGA	AGGATGAC
CAGAAGAAAC	AGATTCAAAAT	TGAATTGAAT	CAGCAGCGT	TACAGATAG	CTGCTCTTA
ACGTTGAACC	CTACAGCTAC	AGAAATGTG	AGCTTCTTT	ATGACAAATA	CTAGAGCGG
TTGACGTTAA	AGACTGGTAC	TGATCGGACA	GAATTAAGG	CAATACGAG	CTGAGCAGCC
GCATCAGCGA	ATGAAGGTTT	AACAGAGAA	GAATTAACAA	ACTCTCTCT	CTGCTGTCG
TCCGAAGAAA	CTGTCGCCAG	CAGCACAACA	GGATAGAAA	GTAAACAAAC	CTGATGACG
ACTGTCAAAAC	CGCGCGTAGC	AGGATCAACA	GATATAGTG	ATTATTTTA	CTGATGAA
ACAACGATTA	TGATAAATTT	TGAAGATCGG	ATTATTTTA	ATTCTGATG	CTGACAGCA
ACACGCCGT	ATAAGAAAGA	TGAGGCAAT	CATTAGAACT	TTGATGGTG	CTGATGAGAA
GATGTGCGAG	AACAAATGAA	AGCAGGCGAT	TAGTTCACT	TTGATTTAG	CTGATTTTG
AAACCTAATA	AACCAAGTTC	AGGTGATTTA	GTTGATGAG	AAGCAATGT	CTATGGAAC
TACACAATTA	GTGAAGATGG	TAGGTTCTG	TTGATTTTA	ATGAGCGAAT	CTGCTGTGAA
AGTGACATTC	ACGGGGACTT	TTGTTTAGAT	AGTATTTTA	ATGATTCAGA	CTGCGGGGGC
CCAGGAGATT	GGGTGATTGA	TATTTCTACA	CAAGAGGATT	TGCGGCTGT	CTGATTTCCA
ATTGTCCAG	ATACCGAACA	ACAAATTTGAT	AAACAAGGC	ATTTTGATG	CTGCGGCAAT
CCTAGTGCGA	TTACTTGGAC	GATGATATC	AATTAAGCA	TGAAAGATGA	CTGATTTCCA
ACTGTGACGG	AAACATGGCC	AAGGGAAT	AGTTTAACT	CGTGAAGAT	CTGATGTTA
GTGATGAATC	TTGATGGAAC	AATTAAGAA	GTGAGGCGG	AATTTAGTG	CTGATTAATAT
ACCGTTGATA	AAAATGGCAA	TGAGGCAAT	AAAGGAGCA	CCACAAAGG	CTGATGCTTT
GAGTACCAAA	CGACGATTGA	CGAGGCGGTT	ATTGAGATG	GCTGGGCGA	CTGCTCTTTT
AAAAATCACG	CGACGTTAAC	AAGGATAAT	AATGGAATG	GGTATGATG	CTGAGCAACT
GTTACCGCCA	CATATGGCAA	AATGTTAGAC	AAGGATA	TAGATTAGG	CTGAGGCAAT
CAAGAATTCA	CTTGGGAAAT	TAACTACAAC	TATGTTAAC	AAGGATTCG	CTGAGGCAAA
GCAGTCATTA	CAGACACAAT	GCGGATAAT	TTAAATTTTG	AAGGATTTG	CTGATATTTA
TATTCAGTGA	CATTTGATGA	CAAGGAAAT	GAAGTCTTG	GATGAGAACT	CTGAGGAGGA
AAAGATTACA	AAGTGGTAAT	CAAGGAGAC	GCTGCTTTG	CAATTTGAT	CTGATATGAT
GTGACTGGCG	CAGTCAAGAT	TGATTTATAA	ACCAAGTTG	ATGGAATTT	CTGAGGCGAT
GTTGCCCGTGA	ATAATCGTGT	GGATGTTGGC	ATGCTGAGC	ATTGAGAGA	CTGATGCGCA
GCCAGTCAAC	AAAATATTAT	TAAAGCACT	GCTGAGTTG	ATTATCAAAA	CTGAGGAGAT
GGTTGGACGT	TAGCTGTGAA	TCAAAATAAT	TATTTTATG	AAAATGCGG	CTGATGCGAT
ACGTACGAAC	CAGTTCTCTG	CTTAAGTATG	GTAGGAAAT	CGTGGTTGT	CTGAGATACA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCACTGGTG	CTCAGTTGAC	GTTAGGCAAG	GATTTTATBG	TAGAAATAAD	TCTTATGCA
GATGGTGAAA	CAGGCTTTAA	GCTAAGTTT	ATAGGTTTBT	ATGGCAAAAAC	AAGTATGCC
TTCCACATAA	CTTATACTAC	CTTTTTTCGAT	GTTATGAAAT	TAGACGCTAA	CAATCTGCG
TTGGACCATT	ATCGAAATAC	CGCTGCCATT	GATTCGATBG	ATGAAACAGG	AAACATCAT
CATTTCAGAAG	ATAGTAAACC	GTTTAAAGCT	TTAGTTTCTT	TTGATTTAAA	TCTGTA AAAA
AGCGGTGTTT	ACAATGCCGT	CACCAAGGAA	ATCAGTTGGA	CGATTGCGGT	TGATTTAAGT
AATAATCGTT	TAGTCGACGC	CTTTTTTGACG	GATCGAATTT	TAAGCAATCA	AACTATTTG
GCTGGGAGCT	TGAAAGTCTA	TGAAGGCAAT	ACAAAGGAG	ATGTTTCGGT	TGAAAGAGTG
AAACCAACGC	AACCGTTGAC	GGATAACACA	ATGGAGAAC	CAAGGAGAA	AAAGGAAAT
ACTTGGCGTG	TTGATTTTCC	TAATGATAGT	CGTATGATG	TGATTGAATT	TAGATGCTCT
GTTGATGAAA	AAGTTATCGA	AGGTTGGGCT	AGTTATGACA	ATAGGCGATC	TGATTA AAAAC
CAAGGTTCTT	CACGTGATGT	GACAGGAAAA	GTTTCTATTC	AACTGCGTG	CAATCTAGTG
AAAAAAGGTG	GCGAATACCA	CAAGGATGAT	CCAGGATGAT	TGTACTGGCA	TGATATGATC
AATGGCGCCC	AATCGGTTTT	AGAGGATGTC	GTTATGATG	ATAGGCGCTC	ATGAAACCAA
GTGCTAGATC	CCGAGTCATT	GCTGATTTAC	GCTAGGAAAG	TAAGGAGAGA	CGGATCTATT
ACGCCAGATA	AATCTGTTAT	TTTGAAGAAA	GGAAAGGATT	ACAGACTGGA	AGTTAGCCACC
GATAATGAAA	CAGGACAACA	AAAAATGTC	GTTAAATGTC	CCCATATTGA	AGGATCTTAT
TATATGGAAT	ATCGTAGTTT	AGTCACTTCT	TCAAGGCGCG	GGATACAGA	CAGGATATCC
AACCAAGTGT	CAATTACTGG	AAATGCTTCA	GAAGTCTTC	ATGGGATGA	CAATGCGAT
GTGGTCGTTG	ACATTGATCA	CAGTGGCGCG	CATGCGAGAG	GGATGAAAG	CAATATTCAG
CTGAAGAAAA	CAGCCATGGA	TGAGAGGACT	ATTTTATGAG	GGGCTATTT	CAATATTTGG
GACCAAGCTA	AAACACAAGT	CGTATGTCBA	GCTAGGATAG	ATGAGACCGG	GATTTTCACA
TTTGGTGGGT	TGCCACAAGG	GCAATACATT	TTGCTGAGAA	CAAAACACCC	ATGAGGCTAT
ACAGTTTCGG	ACGAATTAGC	TAAAGGCGGA	GTCATGATTA	TTGATGAAGA	ATGTTTAGCC
GAAGGAGCAC	AACCAACCAT	TATTA AAAAC	GATGTTAATA	AAGTATTTTT	ATGAAATAATG
GATGAGAAGG	GTA AAAAGTT	AGTCAATGCT	CGTTTGAAT	TAGAGCATGC	CGTATTCACG
CCGTTTACTC	ATTGGGAAGA	AGTTGCGCTT	GGGCTGATTC	GAAGGACGC	GATGCGCCAG
TTAGAGGTGG	ATAGTTTAAA	AGGAGGCTTT	TATCAGTTCA	CAGAAATCGA	AGGATGACAA
GGCTATCTTT	TAGACACGAC	CGGCAAAACGA	TTGATGCTGA	CACAAAATAC	GAGCGGACAA
ATTGCTGATC	TTCATGTCAA	AATGCTTAAT	TACCAAGGTT	CTGCTGAACT	AAATTA AAAA
GACCAAGCAG	GCAATCCATT	AGCAGGTGCT	GAATTTTCTAG	TCCTTACAC	CAGAGGACAA
GCAGTTCGAG	AACACTTAGT	TTGCGATGCA	AACGGAAGAG	TCACAGTGAC	GATTTTAGCC
CCAGGAAAAT	ATCAATTTGT	GAAAGGCAAA	GGGCTGACAG	GGTATCTTTT	AAGCATGAA
CCAAGTGCTT	TCACGATTGC	AGGAAACGAT	CGGCGGAAAC	CAGCAACAGT	TATGTAACG
GCTAATTTTG	TTAATCTATCA	AGGTAACGCT	AAATTAATCA	AAAAAGATGT	GATTTGACAC
TTTATTAAGTG	TGCGACATTT	TAAATGCTTT	GAAGGGAAG	GAGAAACGAT	TGAAATAGGC
TTGACGACAA	ATAATCAAGG	GGAAATGCTT	GCAGATGCTT	TAGGCTCAGG	AAATATCGC
TTTGTAGAAA	CCAAAGCGCC	AACAGGCTAT	TTATTAATA	CCAGGCTAGT	CAATTTTGAA
ATTGCTGAGA	AAAATGCTGG	TAAATGAGCG	GTGCTGCTTG	CTAGTACAA	CTTTGAGAGT
TACAAAGGGG	CTTTCCAAAT	CGTGAAGACG	AATAGGCTAG	ACCAATCATT	AGGATGCTCT
GTTTTTGAAT	TATATGATCA	CAATAAACAA	TCATTAGGGA	TTACAGCAAC	GATGTC AAAA
GATGGCAAAA	TTATCTTTAG	AGACTTGCGG	CCAGGATGCT	ATTATACAA	AGAAATCAAA
GCACCAAAAT	TACCAGATGG	CGCATATAT	ATTATTTATC	CTGAATTAGT	AAAGTAGAA
ATTGCTGGTG	ATTTCAAAGG	TGATGCGGAG	ATTATTTAAT	TAGGCGCTTT	CTGCAATTTT
AAAGGACGCG	CCGTCTTTAA	GAAATTTGAT	GCCAAATGGA	ACCGACTTCC	ATGAAAGATT
TTTAAATTTGT	ATCGAATCGA	AAAGGCGGAA	AAAACTCTTG	AAACAGAAAGT	ATGTTGTCGAA
AAAGATGGTT	CATTGGCTAT	GGAGATTTTA	GGTCTGCTTA	GCTATTAATT	ATGTTGACTG
GATGCAACGG	ATGGCTATAT	CGTCAATAAA	CAACGCTTTT	ATTTTCTAGT	GAGAGGAAAT
TCAATGATA	AACAACCACT	AGATGAGTTA	GAGTTTCTAA	ATTATCAAGC	AGAGGTAATG
GGACGTAAAG	TCAACGAGCA	AGGTAAACCC	TTAGGCTGTC	CAGTTTCTTG	AAATTTCAAT
GCCGATGAGC	AGAATCAGCC	CCAAGGTTCA	CCGATTAAT	TCTTGAATCG	TGAGGAGAA
AAAGTTTCTG	AAATAACAAC	GGATAAGACT	GGGGAATTTT	ACGTTAAAGG	GATTAATGAA
GGGCATTACG	TTTTAGTGGA	AACGAAACCA	CCAAGGCTCT	ATCTGTTAGA	CATTAAGCTTA
CATCCATTTG	ATGTAACCGC	CCAATTAGGA	AAAGAGTASC	CAATGCTTTT	AGTGGATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *Y. E. jaculis* Genes.

ATCAATTATC AAGGACCTCT CAACTAATCT AATCCTATG AAGAGGTGA AATCTGGCA
 GGTGCGGTCT TTAAGGTGAT TCACTAATAA GATCTGCTG TAATGGACA AATCTATCTG
 ATCTCTGACA AAGGAGGCAA AATCTCTG AATCTGCTG TAATGGACA AATCTATCTG
 GTGGAGACAC AAGGAGGCAA TACTATCTCT CTTCTGAAA GGTGAGGCTG AATCTTACG
 ATTGCCAAAG ADAAGCAAGG CAACTAATCT AATCTGCTG TAATGGACA AATCTATCTG
 TACCAAGGCT CTTCTAAGCT GGTGAGGCTG AATCTGCTG TAATGGACA AATCTATCTG
 GAATTTAAAG TCACTAATCT AAGGAGGCTG CAACTAATCT AATCTGCTG AATCTTACG
 AACCAAGGCT TACTTCAAGT CAACTAATCT CAACTAATCT AATCTGCTG AATCTTACG
 AAAGCAGGCT ATCTTCAAGT CAACTAATCT CAACTAATCT AATCTGCTG AATCTTACG
 GCGAAAGACA AACTTCAAGT CTTCTAAGCT GGTGAGGCTG TCACTAATCT AATCTGCTG
 TCCAAAAAAA CAACTAATCT TCACTAATCT AAGGAGGCTG CAACTAATCT AATCTGCTG
 CTTGGTTTAC CCAAAAGCAA CAACTAATCT AATCTGCTG TCTCTTATCT CAACTAATCT
 TTGGTCGGTT TCTCAAGCTG GGTGAGGCTG AATCTGCTG AATCTAATCT AATCTAATCT

EF125-2 (SEQ ID NO:466)

MRKNGPMV NRWLYGLMCL LLVLYSTIL MALASELID
 GQLTLGEVMQ TSQDENTLAL QSKAETCTQE VVTHLWVS INASHWAAPN NIMIQVDDQ
 KKQIQIELNQ QALADTLVLT LNTATEDVT FSYSLALAL TLKGTCTPTE STATSSPAA
 SANEGSTEEA STNSSVPSS EETVASTHA IETCTCTT VETVASTPD IETCTCTDE
 TIIDNFEDPI YLNPCTPAT PPKEDVTH WTHLWVPE VREIMKASDY FIMLPNKL
 PNKPGSGDLV DAEGNLYQTY TISEGCTVRF TENETGSES LINDPFLDT HMTDORGP
 GDWVIDPTQ EDLPFVPI VDETCTIDK QGHTCTPNP SALTCTVDIN QATCTCTNPT
 VTETWPTGNT FKSVMVYELV MNLCTIKEV GRELCTEYT VDKNSNVTIK GCTTHAYRLE
 YCTTIDEAVI PDGGGVPPF NHATLIDNN PNCLCTATV TATCTKMLDK RMLCTEANQ
 EFTWEINYNV GEQTCTKQA VITCTGDNL TFEHCTHLY SVTCTKNE VCTCTVEGK
 DYKVVINGDS SFAIDFLDV TCACTIDVKT KCTCTCTV AVCTCTVGT GCTCTIDGTA
 SQQNLCTNTG AVCTCTCTG WTLCTCTCT LCTCTCTCT YETCTCTCT PCTCTCTCT
 TGAQLTLGKD FMVEITENAL GCTCTCTCT CAACTAATCT HITCTCTCT TCTCTCTCT
 DHYRNTAAID WTCTEAGNNHH SECTCTCT PCTCTCTCT GVNCTCTCT TCTCTCTCT
 NRLVDAPLTD PILCTCTCT GCTCTCTCT KCTCTCTCT PTCTCTCTCT ECTCTCTCT
 WCTCTCTCT TCTCTCTCT DECTCTCT YCTCTCTCT GSCTCTCTCT SCTCTCTCT
 KGGEYHKDDP DCTCTCTCT GCTCTCTCT ICTCTCTCT LCTCTCTCT TCTCTCTCT
 PDKSVILEEG KDCTCTCTCT NETCTCTCT KCTCTCTCT MEYCTCTCT ACTCTCTCT
 QVSITGNGSE VCTCTCTCT VCTCTCTCT ATCTCTCT KCTCTCTCT LCTCTCTCT
 QAKTQVLREG TVDATGVITF GCTCTCTCT VCTCTCTCT VCTCTCTCT ICTCTCTCT
 GAQPTTIKND VCTCTCTCT ECTCTCTCT FCTCTCTCT FCTCTCTCT PCTCTCTCT
 EVDSLKPGLY QCTCTCTCT YCTCTCTCT ICTCTCTCT RCTCTCTCT QCTCTCTCT
 QAGNPLAGAE FSVLDTCTQA VCTCTCTCT GCTCTCTCT GCTCTCTCT PCTCTCTCT
 SAFTIAASDR GKPTCTCTA NCTCTCTCT LCTCTCTCT LCTCTCTCT ANCTCTCT
 TTNNQGEIVA EHLCTCTCT VCTCTCTCT LCTCTCTCT ACTCTCTCT VCTCTCTCT
 KGAFQIVKTN SADCTCTCT FELCTCTCT LCTCTCTCT GCTCTCTCT CTCTCTCT
 PKLPDGADYI IYCTCTCTCT RCTCTCTCT FCTCTCTCT GCTCTCTCT NCTCTCTCT
 KLYRIENGK ICTCTCTCT DCTCTCTCT ACTCTCTCT ATCTCTCT PCTCTCTCT
 NDKQPLDELE FVCTCTCTCT RCTCTCTCT ACTCTCTCT DECTCTCTCT ICTCTCTCT
 VSEITTDKTG ECTCTCTCT HCTCTCTCT TCTCTCTCT PCTCTCTCT ECTCTCTCT
 NYQGTATQTK ENCTCTCTCT AVCTCTCTCT CTCTCTCTCT SDCTCTCTCT NCTCTCTCT
 ETQAPTSYLL NETCTCTCTCT AKCTCTCTCT VCTCTCTCT QCTCTCTCT QCTCTCTCT
 FKVTDAETGQ TVARSLSDN GCTCTCTCTCT PCTCTCTCTCT APTCTCTCTCT AVCTCTCTCT
 KDKPELVNAG FCTCTCTCTCT RCTCTCTCTCT KCTCTCTCTCT GLCTCTCTCTCT YCTCTCTCTCT
 VGLASWLFYK KSKF

EF125-3 (SEQ ID NO:467)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TAACTTTG TTAACATGA AGGCATGCT AANTTAACA AAAAAGATGT GAATGACAC
 TTATTAAGTG GTGCGAATTT TAAATGCTT GATGAGAGG GAGAAACGAT TGAACACAGGC
 TTGACGACAA ATAATCAAAG CGAATTTGTT GCAGATCACT TACCCCCAGG AATATATCGC
 TTTGTAGAAA CCAAAGGCGC AACAGGCTAT TTATTAATA CCAAGCCAGT CCACTTTGAA
 ATTGCTGAGA AAAATGCTGG TAAACCAAGG GTGCTGCTTG CTATGACAA CTTTGTGAGT
 TACAAAGGGG CTTTCCAAAT TGTGAAAGG AATTAACAG ACCAACCATT AGCAGGTGCT
 GTTTTTGAAT TATATGATCA TAATAAADA TCACTTGGGA TTACAGCAAC GACTTGCAAA
 GATGGCAAAA TTATCTTAG AGATTTGGG CCAGTACCT ATTATTACAA AGAATCAAAA
 GCACCAAAAT TACCAGATGG TGCAGATPAT ATTATTCATC CTATATTAGT AATAGTAGAA
 ATTCTGTGGT ATTTCAAAGG TATCCGAGG ATTTTCAAT TATGGCCCTT CCGCAATTTT
 AAAGGACGCG CCGTCTTTAA GAAATTTAT GGCATTCGA ACCTACTTCC AGCAACGATT
 TTTAAATTGT ATCGAATGGA AAACGGGGA AAAATTTTG AAAGAGAAAT AACTCTGAA
 AAAGATGGT CATTGGCTAT GAGGATTTA GTGTGAGTA GCTATGAATT AATGAACTG
 GATGCAACGG ATGGCTATAT GTTCAATAAA CAAGTATTT ATTTGTAGT GAGGAGAAAT
 TCAAAATGATA AACAACCACT AATKAGITA GAGTGTATA ATTATCAAAG AATATAATG
 GGACGTAAAG TCAACGAGCA AGTTTAAAGC TTAGTGGTG CAGTTTTTCC AATTTACAAT
 GCCGATGAGC AGAATCAAGC TAAAGTTCA CGATACAT TCTTGAATCC TGTAGAGAA
 AAAGTTTCTG AAATAACAAC GATTAAGAT GGCATATTT ACCTTAAAGG GCTATATGAA
 GGGCATTACG TTTTAGTGA AATGAAAGCA CCAATGGCT ATCTGTAGA CAGAACGCTA
 CATCCATTG ATGTAAGCCG CCAATTAGCA AAGATGAGC CAATGGCTTT AAGGATCTT
 ATCAATTATC AAGGAATTC TGAATTAAAC AAGAGAACG AAAGAGGTGA AATTTGGCA
 GGTGCGGTG TTAAGTCTAT TATGAAAGA GGTAAACCG TATATGGACA AATCACTG
 ATGCTTGACA AGCAAGGCAA AATCATTTG AAAATTTAG CAGCGGAAC GATTTGTTTT
 GTGGAGACAC AAGCGCCAAC TAGCTATCTT CTAAAGAAA CGGTAAGCGG AATCTTACG
 ATTGCCAAAG ACAACCAAGG CAATCCAGC ACTCTTCTAC TTAAAGCAGC TTTTATTAAT
 TACCAAGGTG CTGCCAAGGT GGTGAAATTT GATCAAAA AGAATGCCTT AATAGGTGCT
 GAATTTAAAG TGACAGATGC AGAGACAGG CAAAGTCTCG CTCTTTCATT AACTTCTGAC
 AACCAAGGGT TAGTTCAAT GATTACTTA CAAGCGGAA AATATACCTT TGTGAAACA
 AAAGCACCGG ATGGTTAGCA ACTCTCTAAG CAAGTCTCG CATTCATAT TGGGCAACA
 GCGAAAGACA AACCTGAAT CTGTAATGG GGCATTTTG TTAACGAGAA ACAAAGCTGA
 TCCAAAAAAA CAAACCAAAA TCAACCAACA ACGAAGCAAG CAGCTAGAGA GAGAGGTGG
 CTTGGT

EF125-4 (SEQ ID NO:468)

NFVNYQGTAK LIKKDVNHL LSCATFFKLD AKGTTQTGL
 TTNNGEIVA EHLAPCKYRF VETRAPICYL LNTTFPFEL AFHAGKPAV VVSDNFVSY
 KGAFQIVKTN SADQPLAGAV FELYDHIFQS IGITFDSGKD GFLIFRDLAP GTTYKKEIKA
 PKLPDGADYI IYPELVFVEI FCFRGEIEI FCLGATANFK GRAVFKKIIA KANPLPGTIF
 KLYRIENGKE IFEREVTAEK LGSLEMLLG AGSYELDEL ATISYIVNFQ FIVEVVKNS
 NDKQPLDELE FVNYQAEVNG KVNNDQGL TL AGAVELIYNA DFQNPQGSF ITTLNRAGEK
 VSEITTDKTG EIIYAGLNEG HYVLETFAP TSYLLTTLH PFIVTAQLGK EGFIALGDLI
 NYQGTALTK ENETGEALAG AVTKVIDETG QIVDGLNLM SDKQSKVIK NLAPEYRFV
 ETQAPTSYLL NETPSASFTI AKDNQYFAT VVLRAPINY QGAAKLVKID QTFVRLAGAE
 FKVTDATGQ TVARSLRSDN GGLVQVHLQ PKKTVETK APDQYQLSFQ AATPTAATA
 KDKPELVNAG TFWNEKQPVV KHTHAPFTT KQAAATGWLK

EF126-1 (SEQ ID NO:469)

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 ATGGTGATTG TCGCTGSAAC AGTTGTSBA AATTTAGTC CCAATTTGGC TTTAGCTGAA
 GAAGCGGTTA AAGCAGSAGA TACAGAAAGG ATGAGTAATA CCGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAAGG GATATTGAAA GGACAGCTA CTTTCCAGT TCAAGCGGT
 GAAACGGAAC CAGTCGATTT AGTATTSTT GAATATCTA GTGGTAGTTT TTAGATAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *Escherichia* Genes.

TTTCACATG TAAGACAAAC AATCATGAA GTAGTAAAG GGTATCTGA TTAACCCG
 GTGATGCTG CTTCATTTT TGAAGAAA CAATATGT TTTTGATG AATGAAAAA
 ATTAATTCAG CTGATTCTA TATTAATG TGAATAA CGCAATGAG TTTATATAA
 AGCCAATTT TGTCTGTTT TGAAGGTT GATAATG GTGATAGG AATGACCA
 GGATTGAAAC TGGCTTAA TAATAAAT TAAATAGG GATATTAA GATGAAAAA
 ACGTATTTCC TATTAAGAC AATAGGCTC GTTAGACAC GTTAGATG TTAATGAT
 AAGACCAATA CCAATATTC AATTAATGA TATGATC CAGACATG TTTAAGTC
 TCAGTGAAT ATAGTATGA CTATAGGT TATAGAC AAGTTTATG GTTAACCA
 GAAATTACTA ACGAAGCTA TGAATGATT ATGATATT GGAAGATT TTAATTTTA
 AGTTCAGTGA ATTCATACTT TGATAAATAT AAAAAGAG TGGATGCTT TTAACACAA
 GAGTTGCAAC AAGGGTATG TATACAGAA GTTATTA CAGTCAATC TATGATGAT
 TTTACAACCC AATTAAAGA AATTTGAAA ATCTATG GGAATGAC AATGAAACA
 GCTTCATTAA GATTTATGA TGAATTTGAT ATTCATGCT GGAAGGCTAG GATGATGCT
 GGAAATGAT TGGCTTTTA AATTAAGGA TAAATTTT TACCAAGTAT TATTAAGGT
 TACGTAGGAA ACATTAAT TATATAGAA GTTAAGAA ATACAGGAT TATACAGCA
 ACCCTTGTA GTAGTATGAC AATTAATGAA CAAATTTG CTAAGGAAT TTAAGCG
 ACGATTCTTA AAAATAGAA TGAATGCTG TATGATGA CGGAGAAAG TTAAGGATT
 ACAAAGATA TGAAGATGA AGAATGCTA GATTAGCA ATCTGAAAG TATTTGAT
 TGGCATGTCA AAACAATTT TGAAGAGAA ATCAATCTT GGAAGCAAG CAGTATGCTG
 GATGACATTA ATAAATGCT AGTATGCTT GATTAAG TGAAGCAAG AATGCTAA
 GATGTTACAG CTAAGTATG AGTAACAGAA AATTAAGCA AAGTAATTT TGAATGAT
 AAACAAGCAG CAGGATGAG TATTTAAGT GATTAAGGT ATTAATGAT TATAGCT
 AAAATTAAAA CTGACGAGAC GGAAGAGAA TGAAGCTT AATTTAAG AATGCTGAT
 CCAACCAAG CCGAGTTAAA GTTATGCAAT AAGTATAG TATTAATTT CAAAGCA
 ACCGTAACAC CACGAGGAT TGAAGCAAT ATTTAAG AAGTATAG AATTAAGCA
 TTAGATTAA CCAAGTGA TGAATATTT AATTAAG TGAAGCA TATTAAGCA
 GAAACAAGCA GTTGAAGCA AGTATGATG TGAAGCA TTAATAAAT GATTAAGCA
 ACTGATGTAA AAGTATGAT TGAAGTATG AATTAAG TGAAGCA TTAATAAAT
 CAAGAAAATA ACAAATAG TATTAAGT AATTAAG CAGACAGCA TTAATTTA
 AGTGGTCATA CGTACAGAT CAGGATGAT AATTAAGT AAGTATAG AATTAAGCA
 GAATTAGCAC CTTATATGTA AAGGATGCT AATTAAGT AAGGATGAT AATTAAGCA
 AACGAAGGTG ACGTATGCA TTTAAGCA AATTAAGT AAGGATGAT AATTAAGCA
 GAAGATCCAA CGATTATGA AGTATGCA AATTAAGT AAGGATGAT AATTAAGCA
 GACCAAGAAT TTAATGCA AATTAAGT AATTAAGT AAGGATGAT AATTAAGCA
 CAAGCCAGCA TGGTATGTA CATTATGTA AATTAAGT AAGGATGAT AATTAAGCA
 GANGAAATG GCAAAATGAT TATATATAT AATTAAGT AAGGATGAT AATTAAGCA
 ACTTTTACTA TGAACAAAA AGATGACAGC TATTTACT TATTTGCTA TATATACCA
 ATGACTATTA CCACTAAAT TAAATGATC AATTAAGT AAGGATGAT AATTAAGCA
 GAACAAGGCG GGATTATGA CCAAGGCTG TTAATTTT GCAAGCAAG TATTTGCT
 CATTCCAACA AGCCAAGCT AAGGCTGCT GCAAGCAAG CAGAGAGCT AATTAAGCT
 GAACCTAAC AACCGTAAA ACGGAAAAA CCGTTACGC CTACAAATCA TTAAGCA
 ACGAACCAG TCAATTTGG AATTAAGCA AATTAAGT AAGGATGAT AATTAAGCA
 ACAACAGTAA ATCAATTTA CAGTATGCA GCTTAATTT TCTTATATG GCTTATGAT
 TTTGGCATAA CAAAAATAA AAAAGAAAA AATTAAG

EF126-2 (SEQ ID NO:470)

MF KKATHLLSTM VIVAGTVGN EPPCLALAEF ATRAGDTEGM TMTVVKDDP
 LADCKRILEG QATFPVAGE TETPLADVE DASGTDNMF PHVQAILEV VLVNQDRV
 MLASYRGGKQ FMFPDGKTKI NSADYDMLR VNTQIYDKS QFVSGFGDVR TGGTPTAPG
 LKLALDITYN THGELTNEKT YFLWTDQVA NTELIYHLK TMTNISINEY PTFHFLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGHEMIN AYWEHESLS SVNRYFLHYK TMTVVKQKE
 LQQGSSSTPED FITSQSIDDF TFLKQVND ELAQTPATA SLTIANGFDI QATATDAG
 NDVPVQINGQ TISATSTESY VGNITLHEV KENTATDAAT LVGGSTNNG TMTVPEPAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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IPKNDNAHAC DVTPEPTTIT KDIENDEHLD LTKRETFPDW HVETAFGNET SCNTASMV
DINKVLDIID VKVTDENBKD VTANSTVTQE NNNVTMMNK QATSYDYLSG HNTTITITTK
IKTDATDEEL APYIEQGGIP NQANLNFONE GNYLEHKPT VTPPPVDPNI ANTHGQEH
DLTNRDQEFK WNVKTAFBNE TSTWTCASMV DNTFTTBIT DVNVTDENGK DWLAKGV
ENNKVTFEMN XQADSYDYLS GHTTNTTITT KIKASTDEE LAFYIEQGGI PHNMLNFGN
EGDVLHSNKP TVTPPAPTPE DFTTKKDIEG QEHLDLTHRD QEFKWNVKA FQNTSTWTQ
ASMVDDINKV LDITDVKVMX ENKHEDVTNG INTDFENKVT FTMNRKDDSY SYLASHITYTM
TITTKIKTDA TDEELAPYIE QNCIPNQADL NFONENSVLH SNKPTVTPPA PTHFEPYKPE
PKQPLKPKKP LPTPNHQAPT NPNHFGKAS KSHLEHTNT TVNPLYMIAG LINDLVAISF
GITKNKKRKN

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EF126-3 (SEQ ID NO:471)

TGAA

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GAAGCGGTTA AAGCAGBAGA TACAGAAAGA ATWAGCAATA CGGTGAAAGT GMAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTGBAA GBACAAAGCTA CTTTCCCAGT TGTAGGGGT
GAAACGGAAC CAGTCGATTT AGTAGTTTBT GAAGATCTTA GTGCTAGTTT TTTAGATAAT
TTTCCACATG TAAGACAAGC GATTEATGAA GTGCTTCAAG GCTTATCTGA TTAAGACCGC
GTGATGCTGG CTTCATATCG CCGCGGAAAA CATTATTGT TTCTGATGG AAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CCGTGAATA CGCAATTGAC TTATGATAAA
AGCCAATTTG TCTCTGTTTT TTAGACCTTT CCGACCTATG GTGTACGGC AATGCGCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAACATACAG GAGATTTAAC GATTTBAAAA
ACGTATTTCC TATTAGTAC ABATGGGCTC GTTATACAC GTTTAGATGG TTAGCTGCAT
AAGACCAATA CCAATGATTC AATCAATGAA TATCTAGATC CAAGACATCC TCTTGAAGTC
TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAATACAG AAGTTTTAGC GTTAAACCAA
GAAATTACTA ACCAAGCCTA TBAATGATT AATBTGTATT GGGAAAGTGT TBAATTTTA
AGTTCACTGA ATTCACTTT TBAATAATAT AAAATAGAAG TGGCTCCTTT TTTAAACAA
GAGTTGCAAC AAGGGICTAG CACACACAAA GATTTTATTA CAAGCCAATC TATGATGAT
TTTACAACCC AATTAAAAAA AATTCTCAAA GATCTCTGG CGCAATCGAC AATGACACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCTATCTG CGACCGCTAC GATATATGCT
GGAAATGATG TGCCTGTTCA AATTAAAGGA CAATATATT CAGCAACTAG TACAGAAGGT
TACGTAGGAA ACATCAGGAT TCACTAGGAA GTTAAAGAAA ATACAGCGAT TBAAT

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EF126-4 (SEQ ID NO:472)

EE AVKAGDTEGM TNTVKVKDIS

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LADCKRILEG QATFPVQASE TEPVPLVWE DASGSPDNF PHVQAIDEV VQGLSDQDRV
MLASYRGKQ FMFPDGHFI NSADYEMINR VNTQLTNDKS QPNSFGDVR TGTGPTAPG
LKLALDTYNQ THGDLTHKFT YFLNLTGVA NTELELHLK TNTNDSINEY PTHHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGHMIN AYVESVESLS SVNSYFDKYK TMTTFVKQE
LQGSSTPED FITSQSIDDF TQLEKIVFD ELAQSTWATA SLTIANQFDI QGATHTDDAG
NDVPVQINGQ TISATSTEGY VGNHTHYEV KENTALL

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EF127-1 (SEQ ID NO:473)

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TAGCGAAAGA AAATAGGGAG CATTAAATG TTTAAAGAAAG CAACGAAATT AGTATCGACA
ATGGTGATTG TCGCTGGAAC AGTTGTGGGA AATTTAGTC CCACATTGGC TTTAGCTGAA
GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAGT GAAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTGGA GACAAAGCTA CTTTCCCAGT TGTAGGGGT
GAAACGGAAC CAGTCGATTT AGTATTGTT GAAGACCTA GTGCTAGTTT TTTAGATAAT
TTTCCACATG TAAGACAAGC EATTEATGAA GTGCTTCAAG GCTTATCTGA TTAAGACCGC
GTGATGCTGG CTTCATATCG TGGCGGAAAA CATTATTGT TTCTGATGG AAGACAAAA
ATTAATTCAG CTGATTATGA TATCAATGTG CCGTGAATA CGCAATTGAC TTATGATAAA

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

AGGCAATTTS TGTCTGATTT TATA AAGCTT TTA A ATG GTTGTAGGCG AGT CCCCCA
 GGATTGAAAC TCGGTTTACA TATA A AAT TTA A ATG GAATTTAAG GAT CAAAAA
 AGBTATTTCG TATTATGAGC ACAA TGTCTT CTTA CAC GTTGTAGATCG TTT TGCAT
 AAGACCAATA CCAATGATTC AAT TATGAA TAT T AATC CAAATACATCC TTT AAGTC
 TCAGTGGAAAT ATAGTAATGA TATA AAGCTT GAT A CAG AAGTTTTAGC GAT CACCAA
 GAAATTACTTA ACCAAGGCTA TGAAT TATT AAT AATT ATT GGGAAAGTCT TTT TTTTA
 AGTTTCAGTGA ATTCATATCT TGAATATCAT AATA AAG TGGTTGCTTT TTT AACAACAA
 GAGTTGCAAC AAGGCTTAC TATA CAGAA GAT TTT TTA CAAAGCAATC TTT ATGAT
 TTTACAACCC AATTAAAAA AATT TAAA GAT TTT TGG CCAATCGAC AAT CCAACA
 GCTTCATTAA CGATTGCGAA TCAATTTGAT ATTAA CTG CCAAGCTTAC GAT ATGCT
 GGAATGATGA TGGCTGTGA AATTAAAGGA TAAA TTT CAGCAACTAG TTT AAGAGGT
 TACGTAGGAA ACATCAGAT TCAGTAGAA GTAA AAA ATAGAGCGAT TTT CAGCA
 ACCCTTGTAA GTAGTGGAC AATGATCAA GAAATTTG CTAGGCAATT TTT AAGCG
 ACGATTCTTA AAAATGACAA TGGT ATGGG TGTAA TGA CAG AGAABA TTT ACGATT
 AAAAAAGATA TCGAAATGA AATA AATTA GAT TTT CCA ATCTGAAAT TTT ATGAT
 TGGCATGTA AAGAGGCTT TGAATAGAA ATAA ACTT GGAAGCAAGC TTT ATGGTG
 GATGACATTA ATAAATGCT AAT TGAAT GAT TTT AAG TCAAGCAGCA AAT TGTAAA
 GATGTTACAG CTAAGCGCA AATATGAA GAAATGAA AAGTAACTTT TTT TGAAC
 AACAAGCAG ACAGGTATGA CTATTTAAT GAT TTT TGT ATAAATGAC TTT TCCACT
 AAAATTAAAA CTGACGGAAC CCAAGAGAA TTT TTT AATTTAATA AAT TGGATT
 CCAACCAAG CCGACTTAAA TTT TGAAT GAT TTT AAG TGTACATT TTT AACCAC
 ACCGTAACAC CACCGCAAT TGT TGAAT AAT TTT AAG AATGAGAAAG AAT AATCAT
 TTAGATTTAA CCAACCGGA TCAAAATTT AAT TTT AAG TCAAAACAG TTT TGTAAAC
 GAAACAAGCA CTTGGAGGA AAGAGGCTG GTAA TGA TTAATAAAT GAT TACATC
 ACTGATGTAA AAGTCAAGA TGAATATCT AAT TTTA CAGTAAACG TTT AATAACA
 CAAGAAAAATA ACAAATGAC TTTTAAATG AAT TTT AAG CAGACAGCTA TTT ATTTTA
 AGTGGTCATA CGTACATAAT GATTTTAT AATATGTA AAGTAGGCT AAT TACGAA
 GAATTAGCAC CTTATATGAA AATATGTA AAT TTT AAG AAGCGACTT GAT TTTGGC
 AACGAAGGTG ACGTGTGGA TTTTAAAGAA CCAAT TAA CAAAGCTG AAT TGTCCA
 GAAGATCCAA CGATTAGAA AATATGGA GAT TTT AAT ATTTAGATTT AAT TACCGT
 GACCAAGAAT TTTAAAGAA TGT TAAAGAA GAT TTT GTA ACGAAACAAG GAT TGTGACC
 CAAGCCAGCA TGGTGTGGA CATTATATA GTTTTGA TCAAGAGACST GAT TTTNCT
 GANGAAATG GCAAAATAT TACATATAT GAT TTT TAA CAGAGAGAAA TTT AAGTA
 ACTTTTACTA TGAACAAAA AGATACAGC TACTTTACT TACTGTGTGA TTT TACACA
 ATGACTATTA CCACTAAAT TAAATGAT GAT TTT AAT AAGATTAAG GAT TATATT
 GAACAAGGCG GGATTGCGAA CCAAGCGAG TTAAT TTT GCAAGAGAG TTT TGTGTG
 CATTCACAACA AGCCAAGCT AAGAGCGCT GCAAGAGAG CAGAGAGAG AATTAACCT
 GAACCTAAAC AAGCGCTAAA AAGGAAAAA CCGTACAGC CTAGCAATCA TTAAGCACA
 ACGAACCAG TCAATTTTGG AAAATCAGCA AGTAAAGAA TTTATTTAGC AAT TACTAAT
 ACAACAGTAA ATCCACTTA TATGATGCA GCTTCAATTG TCTTATAGT GAT TATTAGC
 TTTGGCATAA CAAAAATTA AAAAAAGAA AATTA

EF127-2 (SEQ ID NO:474)

MF KKATKLLSTM VIVAGTVVGN EPTLALAEK AATGSDTEGM TITVKVKDR
 LADCKRILEG QATFPVQAGE TERNLAVVE DAKVDFDNF PHVQAIDEV VVQNDQDRV
 MLASYRGKQK FMFPDQKTKI NSADYEMNVR VVQVLLDKS QFVQSGDVR TTTTPTAPG
 LKLALDTYNQ THGDLTNKRT YFLLVTDGVA NIKVLTGK TTTTDSINER FTTTDLQVS
 VEYSNDYQGA AAEVLALNQE ITNLYEMIN AHWESVSLS SVNIFYDKYK TTTTFFVKQE
 LQQGSSTPED FITSQSIDDF TTQLRQIVKD RLADSDATA SLTIANQFDI QATATDAG
 NDVPVQINGQ TISATSTEGY VGNITTHYEV KENTALLAAT LVSGSTMNQK TTTTFFPEAT
 IPKNDNAHAC DVTPEDPIT KDIENQHL DTHRETFDHW HVKTAFGNET SLTTFASMVD
 DINKVLDIID VKVTDENGKD VTANGVVTQE NHTVTHFNK QADSYDYLSS HTTMTITTK
 IKTDATDEEL APYIEQGSIP NDAENFGNE GCVLHDEPT VTFFPVDPNI AATTTGQEHL

TABLE 1. Nucleotide and Amino Acid Sequence of *E. faecalis* Genes.

DLTNRDQEFK WNVKTAFGNE CTWTTCASNV DDINPNDIT DVKVTDENGE DVTGNGKVTQ
 ENNKVTFEMN XQADSYDYLK QHTYMTTIT KIHACNDEE LANYIEQGGI PKATLNFNGN
 EGDVLHSNKP TVTPPAPTPE DDTTTCNIEE QEHLLTNRD QEPHNVNKTG FGHNSTWTQ
 ASMVDDINKV LDITDVKVKX EHSKVTTEB IVTQELNKKVT FTNKKKDDSV SYLCHTYTM
 TITTKIKTDA TDEELAPYIE QSTTNQACL NFGNENVLH SINKPTVTPPA PFTTPPKKPE
 PKQPLKPKFP LTPTNHQAPT NFWINGKSAK KGIHNTNT TWIPLYMIAG LINDVAISF
 GITKNKKRKN

EF127-3 (SEQ ID NO 475)

GAATCAA GGAACAATTG CTAASSAAT TCAGAAAG
 ACGATTCCCTA AAAATGACAA TCGCATGCG TSTNCTGA CGGAGAGAAGA TCGACGATT
 ACAAAGATA TCGAAAATCA ABAACATCTA CATTAAACCA ATGCTGAAGA TACCTTCGAT
 TGGCATGTCA AAACAGGCTT TSCCAACGA ACGACTACTT GGACCCAAGG CAGTATGGTG
 GATGACATTA ATAAAGTSTT AACTATCATT GATSTTAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AATAAGATAA GAAAATAACA AACTAAGCTT TGAATGAAC
 AAACAAGCAG ACAGCTATCA CTATTTAAGT GGTATACGT ATACAATGAG TATCACCCT
 AAAATTAAAA CTGACGCAAC GAGGAGGAA TTAGGCTT AATTGAACA AGCGGGGATT
 CCCAACCAAG CCGACTTAAA CTTCGCAAT GAAGCTTACG TGCTACATT CAAATAACCA
 ACCGTAACAG CACCGCAAT TATCTCAT ATTTCTAAG ACATAGAAG ACAGAACAT
 TTAGATTTAA CCAACCGCA TAAAGATTT AATTCTACG TCAAAACAG TTTAGTAAC
 GAAACAAGCA CTTGGACCA AACTAGCATG GTATATACA TTAAT

EF127-4 (SEQ ID NO:476)

NQG TIAKEFPEAT

IPKNDNAHAC DVTPEDETIT FDIENQEHLD LTNRETFWDV HVKTAFGNET STNTPASMVD
 DINKVLDIID VKVTDENGHD ATANSTVPE INNVTFPMNK QADSYDYLK HTYMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFNGE GDVLHSNKP TVTPPVDPNI AKTNEGQEHL
 DLTNRDQEFK WNVKTAFGNE CTWTTCASNV IDIN

EF128-1 (SEQ ID NO:477)

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 ATGGTGATTG TCGCTGGAAC AGTTTGGGGA AATTCTATTC CCAATTTGGT TTTAGCTGAA
 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACATATA CGGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAAGG GATATCTGAA GGACATCTTA CTTTCCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCTGATT AGTACTTSTT GAAGATCTTA GTGGTAGTTT TTGAGATAAT
 TTTCCACATG TAAGACAAGG GATTGATGAA GTGCTTAAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTCATATCT GGGCGGAAAA CAATTCTGTG TTTCTGATG AAAAGAAAA
 ATTAATTCAG CTGATTATCA TATGAATCTG CGCGTATATA CGCAATTGAC TTATGATAAA
 AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACCTATG GTGGTACGGC AACCGCCCCA
 GGATTGAAAC TCGCTTTAGA TAGGTAAAT CAAACACACG GAGATTTAAC GAATCGAAAA
 ACGTATTTC TATTAGTGAC AGATCGGCTC GCTAATACAC GTTATGATG TTAATTCGAT
 AAGACCAATA CCAATGATTC AATCAATGAA TATCTATATC CAAGACATCT TCCTTGAAGTC
 TCACTGGAAT ATAGTAATGA CTACCAAGGT GCAGCTACAG AATTTTAGC GTTAACCAA
 GAAATTACTA ACCAAGGCTA TCAATCTATT AATCTCTATT GGBAAAGTCT TGAATCTTTA
 AGTTCACTGA ATTCATACTT TGAATAATAT AAAAATAAG TGCTCCTTT TGTAAACAA
 GAGTTGCAAC AAGGTCTAG CAGACCAATA GATTTCTTA CAGCCAATC TATCTATGAT
 TTTACAACCC AATTAAAAA AATTTCTAAA GATCTCTTGG CGCAATCGAC ACCTGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTTCAT ATTCAATCTG CGACCGCTAC GGAATATGCT
 GGAAATGATG TGCTGTCTCA AATTAACGGA CAAATCTTT CAGCAACTAG TACGAAAGGT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACGTAGGAA ACATCAGGAT TTACTACGAA GTCAAAATAAA ATACAGCGAT TGAGCCAGCA
 ACCCTTGTA GTAGTGGGAC AATCAATCAA GGAACGCTTG CTAAGGAATT TCGTGAAGCG
 ACGATTCCCTA AAAATGADAA TGGGATGCGG TGTGACCTGA CGGAGAGAAGA TCGAACGATT
 AAAAAAGATA TCGAAAATGA AGAAGACTTA GATTTCACCA ATGCTGAAGA TACTTTGAT
 TGGCATGTCA AAACAAGCTT TGGTAAGGAA AGGAGCTT GGACCCAAGC CAGATGGTG
 GATGACATTA ATAAAGTGGT AGAATTCATT GATTCAGGAG TCACCGACGA AAATGCTAAA
 GATGTTACAG CTAACGGGAC AGTAACACAA GAAATACAA AAGTAACCTT TGAATGAAC
 AAACAAGCAG ACAGTATGGA CTATTTAAAT GTTATGAGT ATACAATGAC TATTAACACT
 AAAATTAAAA CTGACGCAAG GGACCAAGAA TTAGGCTTT ACATTGAACA AGATGGGATT
 CCCAACCAAG CCGACTTAAA GTTTCGCAAT GAAGCTTACG TGTTACATTC CAGTAAACCA
 ACCGTAACAC CACCGGAGT TCAATGAAAT ATTGCTGAG AGGTAGAAGG AATGACACAT
 TTAGATTTAA CCAACCGGCA TCAAGAAATT AAATGGGACG TCAAAACAGC TTTCGTAAC
 GAAACAAGCA CTTCGACGCA AGGTAGCATG GTATATACAA TTAATAAAGT GTTACACATC
 ACTGATGTAA AAGTCACAGA TGAAGATGCT AAGCATCTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAAATA ACAAAGTAAC TTTCGAAATG AAGCAATGAG CAGACAGCTA TGAATATTTA
 AGTGGTCATA CGTACACAAT GAGCATTAAT ACTAAATGCA AAGCTAGCGT AAGTACCGAA
 GAATTAGCAC CTATATTTGA AAGAGGTGCT ATTTCGAAAC AATCGGACTT GAAATTTGGC
 AACGAAGGTG ACGTGTGGA TTTCGAAACAA CCAAGCTTAA CATTACCTGT AAGTACCGCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GCGCAAGAAC ATTGAGATT TAAATACCGT
 GACCAAGAAT TTAATGGAAT GTTCAATACA GTTTCGCTA ACGAAACAAG CAGTTCGACC
 CAAGCCAGCA TGGTGGATGA GTTTCGCTA TCAAGACGCT GAGTCTNCT
 GANGAAATG GCAAAGATCT TCAAGATTAAT GGCATCTTAA CACAAGAAAA TATTAAGTA
 ACTTTTACTA TGAACAAAAA AGATACAGAC TACTCTTACT TACTTGCTCA TATATACACA
 ATGACTATTA CCACTAAAAT TAAAGCTGAC GCAACGATG AATAATTAGT GGTATATATT
 GAACAAGGCG GGATTCCCA CCAACCGGAC TTAACTTTG GCAACGAAG TTAGCTGTTG
 CATTCCAACA AGCCAACCGT AACACCGGCT GCAATACGCT CAGAGACCG AATTAACCT
 GAACCTAAC AACCCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCAGCA
 ACGAACCCAG TCAATTTTGG AAAATGACGA ACTAAAGAA TTTATTTTAC AATTAATAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GCTTTGCTG TCCTTATAGT GGTATTAGC
 TTTGGCATAA CAAAAATAA AAAAAAGAAA AATTAG

EF128-2 (SEQ ID NO:478)

MF KKATKLLSTM VIVACTVVGK FQPTLALALE AVIAGDTEGM INTVKVKDES
 LADCKRILEG QATFPVQAGE IEFVLLVVE IASSSIENF PHVFQAIDEV VQRLCEQDRV
 MLASYRGGKQ FMFPDGKTHI NSADYDNNVR VNTLNTYKS QFVSGFGDVR TYSTPTAPG
 LKLALDYNQ THGDLINFKT YFLNTEGVA NTRLDGVHKK TMTNDSINEY PEPHPLQVS
 VEYSNDYQGA AAEVLALME IEFVLLVVE IASSSIENF PHVFQAIDEV VQRLCEQDRV
 LQQGSSTPED FITSQSIDCF TTQLHQIVKD FLA, STATA SLTIANQFII QSATMTDDAG
 NDVPVQINGQ TISATSTEGY VGLITIHVEY FENTAILAAT LVSGGTMNQ3 TIAHEFPEAT
 IPKNDNAHAC DVTPELFTIT FDIENKEFLD LTHNEHFDW HVPTAFGNET STWIASMV
 DINKVLDIID VKVTDENGFD VTANGTITQE IHHNTFEMK QAFSYDYLEG HTYMTITTK
 IKTDATDEEL APYIEQGGIP NCADLNFGNE GDIHSELEPT VTFFPVPDNI AFDIEGQEHL
 DLTNRDQEFK WNVKTAFGNE TSTNQASMV DDINKVLEIT DVIVTDENGK EVTANGKVTQ
 ENNKVTFEMN XQADSYEYLS GHTYTHITTT HEPKATDEE LAPYIEQGGI ENQDLNFGN
 EGDVLHSNKP TVTPPAFTPE DFTITHIEIG QEHLDINRD QEPHWNVFTA FGNMTSTWTQ
 ASMVDINKV LDITDVVXX ENHFWTENG INTEHMKVT FTHMKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGSIHQADL HEGHKKVHLH SNKPTVTPPA PTFEDIKKPE
 PKQPLKPKKP LTPTNHQAPT NPMHFKSAS KGIHLEHNT TWPPLYMIAG LITVVAISF
 GITKNKKRKN

EF128-3 (SEQ ID NO:479)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes

AGA TGAAAATGGT AAAGATGTTT ATTTAAG TTTTAACTTAACA
 CAAGAAAATA ACAAAGTAAC TTTTAAAGT AATTTTAAAG GAAACAGCTA TTTTATTTA
 AGTGGTCATA CGTACAAAT GATTTTAAAT TTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAATTAGCAC CTATATTTGA AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 AACGAAGGTG AGTGGTGGT TTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAAGATCCAA CGATTACAAA AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GACGAAGAAT TTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 CAAGCCAGCA TGGTGCATGA GATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GANGAAAATG GATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 ACTTTTACTA TGAACAAAAA AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 ATGACTATTA CGACTAAAAA AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAACCAAGCG GATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 CATTCACACA AGCCAAAGGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAACCTAAAC AAGCGTAAAC AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 ACGAACCAG TGAATTTTGG AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT

EF128-4 (SEQ ID NO:480)

DENGK DVTANGKVTQ

ENNKVTFEMN XQADSDYLS DNTTNTTITT HNTTNTTTEE LATTIEQGI FNTTNTNFGN
 EGDVLHNSKP TTPPTPTPE DNTTNTTTEE HNTTNTTTEE LATTIEQGI FNTTNTNFGN
 ASMVDINKV LNTTNTTTEE HNTTNTTTEE HNTTNTTTEE LATTIEQGI FNTTNTNFGN
 TITTKIKTDA TDEELAPYIE DNTTNTTTEE HNTTNTTTEE LATTIEQGI FNTTNTNFGN
 PKQPLKPKKP LTPTNTTTEE HNTTNTTTEE HNTTNTTTEE LATTIEQGI FNTTNTNFGN

EF129-1 (SEQ ID NO:481)

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 ATTGCTACCC CAAGCATCGG TTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 CAAGAAATTT CATCATTTAA AGCAAAACAA GGGGATTTAG CTTCACAAGT ATTTTCTTTA
 GAAGCAGAAG TATCTTCAAGT ATTTTATGAA AGATTTCTT TACGTGAAGA AATTTTAAACA
 CTAAAGCAA AATCASAACA ATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 AAACGTAACG AAGCAATCAA AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 ACAATGCTAG ATGCAATTTT AGATTTTCAAG TCAATTTCAAG ATGCAATCAG CTTCATTTCAA
 GCTGTTTCAA CAATCGTAAG TGGCAACAAC GATTTTATG AATTTTAAACA AATTTTAAACA
 CAAGCCGTTG TTATATAAAA AGTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAAGCTGAAT TAGAAACAAA AGTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 ATGAAAGCTT CATTAGCATT AGAATTTCA TCAATTTCAA GTTCTAAAGT TCAATTTCAA
 AAACAAAAG CAATCTGTA AGCAAGCAAG GATTTTATG CTGCTGAAGA AATTTTAAACA
 GCTGAAAAG CCAAAACAGT TGGTAAACAA GATTTTATG CTGCTGAAGA AATTTTAAACA
 CCAGTTGCCT CTTCATCAA AGCAAGCAAG GATTTTATG CTGCTGAAGA AATTTTAAACA
 GAATCAAGCA CGCAACAAA AGTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAAAATACTG GCTCTTTTTC ATCAGAAACA GATTTTATG CTGCTGAAGA AATTTTAAACA
 GGAAATAATG GTTCTTAAAC TGGTAAACAA GATTTTATG CTGCTGAAGA AATTTTAAACA
 GCGCCTTCTG CTATATCAA AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 CGTCCAGTAG TATGGGATG AGTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 GAAGCAGGTG GATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 TGGGCGCCAG GTAATCTAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 TCAGGAAGCG GTCACCTGA TTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT
 TACTCAGGTA GATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT AATTTTAAAGT

EF129-2 (SEQ ID NO:482)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VKKRLFASV LLCSLTLSAI ATPSLALADN VDFNHHHMQ EISSLKAKQG DLASQWSSLE
 AEVSSVFDES MALREQKQTL HAKSEQLQOE ITNLMHIEK RNEAIKNQAR DVQTHNQSTT
 MLDAVLDDADS VADAISEVQA VSTTFNANNE LMQTHHEKQ AVVDKKAENE KHYVPLEATE
 AELETKRQDL LSKQSELNVM HAKSLALEQSS AESSHAELEF QKAAAEAEQA ELAAHKKAAA
 EKAKQAAAKP AKAEVKAEAP VASSSTTEAQ APASSSATE SSTQQTTEET TPSTTHSATE
 NTGSSSSEQP VQPTTPSDNG NHGSGTGGGT VPTTHHHPA PSADPTINAL NVLRHFLGLR
 PVVWDAGLAA SATARAAQVE ACCINHHWS RGEFVHIMW APGNSVIMAW YNEHHTVTAS
 GSGHRDWEIN PGITRVGFGY SSTTHGHSA

EF129-3 (SEQ ID NO:483)

GGAC AATGTTGATA AAAAAATTGA AAAAAAAAT
 CAAGAAATTT CATCATTAATA ATTAAAAATA GGGGATTTAG CTTTACAAGT ATGTTTCTTA
 GAAGCAGAAG TATCTTCAGT ATTTGATGAA AGCATCGCTT TACGTGAACA AAAACAAACA
 CTAAAAGCAA AATCAGAACA ATTATACAA GAAATTAACA ACTTGAATCA AGGTAATTGAA
 AAACGTAACG AAGCAATCAA AAATCAASCA CEGATATTTT AASTTAATGG AAAACACACA
 ACAATGCTAG ATGCAGTTTT AATATCGGAC TGAATTTAG ATGCAATCAG CCGTCTTCAA
 GCTGTTTTCAA CAATCGTAAG TGGGAAACAC GATTTAATGC AACACACAAA AGAABACAAA
 CAAGCCGTTG TTGATAAAAA AATTGAAAC GAGAAAAAG TGAACAACT TGAACCAACA
 GAAGCTGAAT TAGAAACAAA AATTGAAAT TTACTTCTTA AACAATCTGA ATTAAACGTA
 ATGAAAGCTT CATTAGCATT ABAACAATCA TCGCTGAAA GTTETAAGG TGGTTAGAA
 AAACAAAAAG CAGCTGCTGA ABAAGACAAA GTACCTTAG CTGCTGAACA AAAAGCTGCA
 GCTGAAAAAG CCAACAAGC TGTTCGAAA CCGCTAAG CTGAAGTGA AGTAAGCA
 CCAGTTGCCCT CTTTATCAAC AATAGAACCA CAACGACGAG CAACCTCAAG CTGAGCAACT
 GAATCAAGCA CGCAACAAC AATTGAAACA ATTACACAA GTAGAGATA TAGTCAACA
 GAAAAATACTG GCTCTTCTTC ATCAGAACCA CCACTACAC CTATACACG AAGGATAAT
 GGAAATAATG GTGGCCAAAC TGTGTTGCA ATAGTTACAC CAACACCAGA ACCACACCA
 GCGCCTTCTG CTGATCCAAC AATCAATGCA TTGAAGCTTC TACGTCAAT ATTACTTTA
 CGTCCAGTAG TATGGGATGC AATTGTTGCA GTTCTGCA CTGCTCGTGC AGCAAGTT
 GAAGCAGGTG GCATTCCAAA TATGACTGAG TTTGCTGAG ATGAGTTAT CGCAATTATG
 TGGGCGCCAG GTAACACAGT AATCATGCG TGGTAATG AAACAAACAT GTTACAGCT
 TCAGGAAGCG GTCACCGTGA TTGGAATTT AAGCAAGTA TTACGCGTGT CGCTTTTGGT
 TACTCAGGTA GCACAATCGT AGGACACTCA GGC

EF129-4 (SEQ ID NO:484)

DN VDKKIEEKQ EISSLKAKQG DLASQWSSLE
 AEVSSVFDES MALREQKQTL HAKSEQLQOE ITNLMHIEK RNEAIKNQAR DVQTHNQSTT
 MLDAVLDDADS VADAISEVQA VSTTFNANNE LMQTHHEKQ AVVDKKAENE KHYVPLEATE
 AELETKRQDL LSKQSELNVM HAKSLALEQSS AESSHAELEF QKAAAEAEQA ELAAHKKAAA
 EKAKQAAAKP AKAEVKAEAP VASSSTTEAQ APASSSATE SSTQQTTEET TPSTTHSATE
 NTGSSSSEQP VQPTTPSDNG NHGSGTGGGT VPTTHHHPA PSADPTINAL NVLRHFLGLR
 PVVWDAGLAA SATARAAQVE ACCINHHWS RGEFVHIMW APGNSVIMAW YNEHHTVTAS
 GSGHRDWEIN PGITRVGFGY SSTTHGHSA

EF130-1 (SEQ ID NO:485)

TGATACATTA AAAGGAGGGA AATATGCGC CCAAAAGAGA AAAAAAGAGG AAAAAATTGG
 TTAATCAACA GTTTATTAGT TTTATATTT ATCATGGCT TAGCCTTAAT TTTTACAAT
 CAGATACGTA GTTGGGTGGT TCAAAAAAT AGCGGTGGT ACGCCGTTAG CAAGTTGAAA
 CCAGCTGATG TGAAGAAAAA TATGCTGCT GAACACAGT TTACTTTGA TTCTTTGAG
 TCCTTGAGCA CAGAAGCGGT GTGGAAGGC CAATTTCAAA ACAAAAACCTT ACCTTGATT
 GGTGCCATTG CGATACCAAG TGTCAAAAT AATTTTCCA TTTTAAAGG ATTATCAAT
 GTCGCTTTAT TAACTGGTGC TGGGACCATG AAAAATAAT AAGTCATGS GAAATCAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *Elaphoglossis* Genes.

TATGCCTTGG CTAGTCATCG AAGGAAATCT GATGATCTT TATTTTCAGT TTTTAAAAGA
 ACCAAAAAAB AGCAACTCAT TATATTAATC GATGATCTT CTGTTTATAT ATTTTAAATA
 ACTTCTGTAG AAAAAATCGA AATATTAATC GATGATCTT TTTTAAAAGA TTTTATGACG TTTTATGACG
 AATATGATTA CCTTAATTAC GATGATCTT GATGATCTT GATGATCTT TTTTATGACG TTTTATGACG
 GGAACATTAG CAGCAACGAG GATGATCTT GATGATCTT GATGATCTT TTTTATGACG TTTTATGACG
 CAATTGGAGC AAAAAACTTT AATATTAATC GATGATCTT GATGATCTT TTTTATGACG TTTTATGACG

EF130-2 (SEQ ID NO:486)

YIKRRENMRP KEKKRNNWL INSLKLLFI IYKALFNNQ IRSWVVQONS FSWKSKLKP
 ADVKKNMARE TTFDFDSVES LSTDAVNNAG FENKNNWIG AIAIPSVEIN LPINNLSNV
 ALLTGAGTMK EDQVMGNVY ALASHRTEDG NLSKNNHRT KKDELIIYID LSTNTYKIT
 SVEKIEPTRV ELIDVPGQN NITLITGDL GATGATCTT TLAATTPIKD ANNNELKAFQ
 LEQKTLADWV A

EF130-3 (SEQ ID NO:487)

CGTTAG CAAGTTGAAA
 CCAGCTGATG TGAGGAAAAA TATGATCTT GATGATCTT TTTTAAAAGA TTTTATGACG
 TCCTTGAGCA CAGCAACGAG GATGATCTT GATGATCTT AAAAAACTT AGGATGATG
 GGTGCCATTG CGATAGCAAG TATGATCTT AATATTAATC TTTTAAAAGA TTTTATGACG
 GTCGCTTTAT TAAGTCTTGC GATGATCTT AATATTAATC AAGTCATGCG GATGATCTT
 TATGCCTTGG CTAGTCATCG AATGATCTT GATGATCTT TATTTTCAAG TTTTAAAAGA
 ACCAAAAAAG AGCAACTCAT TATATTAATC GATGATCTT CTGTTTATAT ATTTTAAATA
 ACTTCTGTAG AAAAAATCGA AATATTAATC GATGATCTT TTTTAAAAGA TTTTATGACG
 AATATGATTA CCTTAATTAC CTGTTTCAAG TTTTAAAAGA CAGCAACGAG TTTTATGACG
 GGAACATTAG CAGCAACGAG GATGATCTT GATGATCTT GATGATCTT TTTTATGACG TTTTATGACG
 CAATTGGAGC AAAAAACTTT AATATTAATC GATGATCTT GATGATCTT TTTTATGACG TTTTATGACG

EF130-4 (SEQ ID NO:488)

VSKLKP
 ADVKKNMARE TTFDFDSVES LSTDAVNNAG FENKNNWIG AIAIPSVEIN LPINNLSNV
 ALLTGAGTMK EDQVMGNVY ALASHRTEDG NLSKNNHRT KKDELIIYID LSTNTYKIT
 SVEKIEPTRV ELIDVPGQN NITLITGDL GATGATCTT TLAATTPIKD ANNNELKAFQ
 LEQKTLADWV A

EF131-1 (SEQ ID NO:489)

TAGGCGGAGG TAAGCGGTAT GGTAAACGAG GATGATCTT AAGACATGAG AATATGAAT
 TGGCTTTTTA TAGTATGTTT GTTGTGCTG AATATGCTA GTGGTTATTT AATAAAAACG
 TTCTTTTTC AATAGATTTT AATATTAATC GATGATCTT AAGTGGTCTT GATGATGAT
 CGCCGAAGTG ATAATTATG GATGATCTT AATATTAATC TTTTAAAAGA TTTTATGACG
 CTTGATCAAA AATATTAAG AATATTAATC AATATTAATC CTTGATCTT TATGATGAT
 CAGGTTTATG TAAATTAAGG ATATGCTTGT GATGATCTT AAAAAACTT AGGATGATG
 CCAACACAA GGTTTTATG TTTTAAAAGA GATGATCTT TTTTAAAAGA CTTGATCTT
 AAAGCAATTG AAGAAAGTAA AATATTAATC GATGATCTT TTTTAAAAGA CTTGATCTT
 ATTCAAGGTG CTGAGATAT TATGATCTT GATGATCTT AATATTAATC TTTTAAAAGA
 TTATCAGCAA TGCTTAATAA TATGATCTT GATGATCTT TTTTAAAAGA CTTGATCTT
 AATACCATTC AAGTCAATAA AATATTAATC AATATTAATC CAGTAAATTT TTTTAAAAGA
 GCAGGAATGT TAGAGAAAAT GATGATCTT AATATTAATC AATATTAATC TTTTAAAAGA
 CACAAAACGG CTGTTTAAA GATGATCTT TTTTAAAAGA CTTGATCTT AATATTAATC
 AATCAACAA GTTATAAATG AATATTAATC AATATTAATC AATATTAATC TTTTAAAAGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCAGCTAGTT TTGCCATGA ATCTTCACT GCTATCTGGG ATATGACGAC AGCTGATTTG
 TATTGGTACT TACATCAATT AACTATGGA CATTAGTTT CCACCGCACT TTTCAAAAA
 TTATGGACGT CTTCTCAGCA AAGCTTTAT CATATGGA TCTATGTTCA TGATTAATTAT
 TTACGTTTAC ACGGCGTTGA AGCGGTGCA CAATCTGGG TTTTATTTTC AAAGCATATG
 AAGACAGGGG TCATATTGCT AACTAATGT GTAAATGAG CGAAATACAA AGAATTAATT
 GGTTCGTTGT TCCATGATGT AACTAATTTA ACTTAAAT TTAA

EF131-2 (SEQ ID NO:490)

MRKRH AKKRHGGVNW LFIVCLLWV GSGYLKTF EFTRDSQVSQ ESKVVLKED
 RSDNYANLTK EIVAPDSGEL DQKIQETWYI GSALIHEDQ VLVNKGYGFA NFFNQANTP
 NTRFQIGSIQ KSFTTTLILK AIEBKRLTD THTATWQI QGAEDITISD MLNHTSGLKL
 SAMPNNIVTD EEIIQFVKQN TIQNKGYKN YSNKULLA CMLEKMYQRT YQLENNLYH
 KTAGLKNFGF YETLLEQPNN STSFWTEEN SHKULIPA ASFAHEFGTG NVLHTGDLY
 WYLHQLTSGH LVSTALLQKL WTSSQSSYH GGTWTHYL RLHGVEAGQQ ALNLEKDMK
 TGVILLTNCV NPAKYKELIG SLFHWTLNLT VK

EF131-3 (SEQ ID NO:491)

TTT AATAAAAACG
 TTCTTTTTCA CTAGAGATTC ACAATTACT CAAATCTGA AAGTGGTCTT GGAAGAAGAT
 CGCCGAAGTG ATAATTATGC GAATTTAAGG AATAATAG TTGCACCAGA TAGTGGCGAA
 CTTGATCAAA AAATTCAAGA AACAATTAT ATTCTTGGG CTTTGATCAT TATGATGAT
 CAGGTTTTAG TAAATAAAGG ATATGGCTTF GGAATCTTG AAAAGCAACA AGCGAACACG
 CCAAACACAA GGTTCAGAT TGCCTCAATT CAAATCTT TTACCACAC CTGATCTTA
 AAAGCAATTG AAGAAAGTAA ACTTACATTA GATACAAAAC TCGCTACGT TTATCGCGAA
 ATTCAAGGTG CTGAGATAT TACGATTAGC GATCTTTGA ATATGACAAG TGCTTAAAG
 TTATCAGCAA TGCTAATAA TATCTTATC GATCAACAAA TTATTCAATT TCTTAAACAA
 AATACCATTG AAGTCAATAA AGGAAAATAC AATTATCTCC CAGTAAATTT TCTCTTTTA
 GCAGGAATGT TAGAGAAAAT GTATCAACGT AGCTATCAG AATTATTTAA TAATCTTAT
 CACAAAACGG CTGGTTTAAA GAATTTTGGC TCTATGAAA CCTTATTGGA ACAGTCAAT
 AATTCAACAA GTTATAAATG GACAGAAGAT AATCTATA ACCAAGTGT CTCATTCCT
 GCAGCTAGTT TTGCCATGA ATTTGGACT GCTATCTGG ATATGACGAC AGCTGATTTG
 TATTGGTACT TACATCAATT AAGGAGTGA CATTAGTTT CCACCGCACT TTTCAAAAA
 TTATGGACGT CTTCTCAGCA AAGCTCTTAT CATTCTGGA TCTATGTTCA TGATTAATTAT
 TTACGTTTAC ACGGCGTTGA AGCGGTGCA CAATCTGGG TTTTATTTTC AAAGCATATG
 AAGACAGGGG TCATATTGCT AACTAATGT GTAAATGAG CGAAATACAA AGAATTAATT
 GGTTCGTTGT TCCATGATGT AACTAATTTA ACTTAAAT TT

EF131-4 (SEQ ID NO:492)

LIKTF EFTRDSQVSQ ESKVVLKED
 RSDNYANLTK EIVAPDSGEL DQKIQETWYI GSALIHEDQ VLVNKGYGFA NFFNQANTP
 NTRFQIGSIQ KSFTTTLILK AIEBKRLTD THTATWQI QGAEDITISD MLNHTSGLKL
 SAMPNNIVTD EEIIQFVKQN TIQNKGYKN YSNKULLA CMLEKMYQRT YQLENNLYH
 KTAGLKNFGF YETLLEQPNN STSFWTEEN SHKULIPA ASFAHEFGTG NVLHTGDLY
 WYLHQLTSGH LVSTALLQKL WTSSQSSYH GGTWTHYL RLHGVEAGQQ ALNLEKDMK
 TGVILLTNCV NPAKYKELIG SLFHWTLNLT VK

EF132-1 (SEQ ID NO:493)

TAGTTTTCTAATCTCACCAAAACAAAATTTTTTAAAGAGGAGATCGTTATCTAGAAAATGGAAAGTAGTA
 GTGGGAAGTCTGGGAATGTTGATCTCTTTTATATCTAGGCGATGTTCAACAAATTAAGACAAAAGATACAGTG

TABLE 1. Nucleotide and Amino Acid Sequences of *B. tularensis* Genes

[illegible]

EF132-2 (SEQ ID NO:494)

[illegible]

EF132-3 (SEQ ID NO: 435)

ATGTTCAACAAATAGTAAGAGCAAAATATAGTGTGTTTATGAGAAAAATTAAAGGTAATGTTTACTAATTTCGATTTT
AGCAGATATTACTGAAAATATAGCAGAAAATATAAAATATGTTTACACASTATCCTACCTTATGGGAAAGATCCCCACGA
ATATGAACCTTTTGCGGTGAAATATGTTTAAATAACTTAAATACAGATTGTGATTCTTTATTAATGGTGTTAACCTTGGAmAC
TGGAGGAAATGCTTGCCTTTACAAAATTATGTA AAAATGACAAAAGGAGAAACAAAATTTATTTTGCAGCAAGTGA
TGGCATAGATGTTTATTTACTTAGAATTTGTAAGTGTGTTTATGGAAGGAAAGATCCCTCTCTGTGTTAAATTTAGAAAA
CGGTATTATTATTCGCTTAAAAATATTCAAAATGCTTAAATGAAAAAGATCCTTATAATTAATAAATTCATATAAGAAAA
TCTAGATAAGTATATTGAAAAGTTTAAATCTCTAGTAAATGAAAGCTAAATCTAAATTTCTTCAATTCCGAATGATAA
AAAAATGATTGTTTCAAACTGAAGGATTTTAAATGCTTATGGAAGGCTATATCTCTCTCTGCTTACATTTGGGA
AATCAACACTGAAGAAGGAACAATGATGAATTAATGCTTACCTAGTGA AAAATTTATGACAAACAAAAGTTCCCTC
CTTATTTCGTAGAAAATAGTGTGGAATATAGACCGAATGCTTATGATATCAAAAATATATCTTATTCCCTATCTATTCAAC
GATTTTTTACTGATTCAATTTGCACAAAATGACAAAGTCTATAGTTTACTATCTGATTTTAAATGGAACCTGGATAA
AATTGCTGAAGGCCTTTGAAA

EF132-4 (SEQ ID NO:496)

CSNSTSKDKDVTASNEKLKVVTNSILATITERIAFVITLSSVPIGKDPHEHYEPLPEVTKTSKADLIFYNGVNLXT
GGNAWFTKLKVXKANKEENKDYFAASDSDITYLEGRVITVEDPHAMNLNENCIYANFIEHWLAEKDPDNKKFYKEN
LDKYIEKLDSDLKEAKSEFASIPNLIWITVSEGGVITVAVNVPSAYIWEIITEEIVLSDQIKHLVEKLRTTKVPS
LFVESSVDDRPMKTVSKDTHIFINLITINIAEKNLITVYAMKKNLNDKIEGSL

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

Query	GenBank Access. No.	GenBank Gene Description	BLAST Score	BLAST P-Value
EF002-2	gi 2338759	(AF018073) periplasmic sorbitol-binding protein; SmoE [Rhodobacter	113	3.60E-18
EF003-2	gi 1552773	hypothetical [Escherichia coli] >gnl PID[d1012634 hypothetical 29.4	278	1.20E-53
EF003-2	gi 2196996	lipoprotein homolog [Treponema pallidum] ~gi 2108234 29K protein	309	3.30E-44
EF003-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	263	9.20E-40
EF003-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	197	2.10E-39
EF003-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	197	7.80E-39
EF003-2	gi 2314748	(AF000654) outer membrane protein [Helicobacter pylori]	263	4.60E-37
EF003-2	gi 349530	lipoprotein [Pasteurella haemolytica] ~gi 50508 lipoprotein	189	4.10E-29
EF003-2	gnl PID[c118135]	similar to hypothetical proteins [Bacillus subtilis]	158	2.70E-26
EF003-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	200	1.20E-25
EF003-2	gi 1336657	lipoprotein [Bacillus subtilis]	182	2.70E-25
EF003-2	gnl PID[e233873]	hypothetical protein [Bacillus subtilis] >gnl PID[e1182900	186	1.30E-23
EF003-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	199	6.60E-23
EF003-2	gi 349531	lipoprotein [Pasteurella haemolytica] ~pir JN0752 JN0752 outer	198	1.30E-20
EF003-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	198	1.80E-20
EF005-2	gi 537235	[Kern Rad1 identifies as gpmB [Escherichia coli] ~gi 1790856	127	6.20E-12
EF006-2	gi 1552773	hypothetical [Escherichia coli] >gnl D[d1012634 hypothetical 29.4	255	1.40E-60

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF006-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	221	6.40E-49
EF006-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	283	2.70E-48
EF006-2	gi 2196996	lipoprotein homolog [Treponema pallidum] >gi 2108234 29K	267	4.40E-47
		protein		
EF006-2	gnl PID e118435	similar to hypothetical proteins [Bacillus subtilis]	359	1.80E-44
EF006-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer	218	3.80E-41
EF006-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	220	2.30E-38
EF006-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	193	2.60E-38
EF006-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	218	1.20E-36
EF006-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	112	8.50E-34
EF006-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	112	1.50E-33
EF006-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	114	1.30E-29
EF006-2	gi 294069	lipoprotein 1 [Pasteurella haemolytica]	114	1.20E-27
EF006-2	gi 1336657	lipoprotein [Bacillus subtilis]	202	3.00E-26
EF006-2	gnl PID e233873	hypothetical protein [Bacillus subtilis] >gnl PID e1182900	200	6.50E-25
EF008-2	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	1590	2.70E-211
EF008-2	gi 393269	adhesion protein [Streptococcus pneumoniae]	986	1.80E-129
EF008-2	gi 153834	adhesin specific for salivary pellicle of dental surfaces	973	1.00E-127
EF008-2	gi 1575030	surface adhesin A precursor [Streptococcus pneumoniae]	934	2.00E-126
EF008-2	gi 153826	adhesin B [Streptococcus sanguis] >pidA 43583 A43583 adhesin	916	3.90E-126
		B		
EF008-2	gi 1184932	36kDa [Streptococcus cristae]	913	3.30E-123
EF008-2	gi 1117994	surface antigen A variant precursor [Streptococcus pneumoniae]	917	5.60E-124

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF008-2	gi 310633	adhesin [Streptococcus gordonii]	891	6.00E-122
EF008-2	gn PIDe255529	lipoprotein [Staphylococcus epidermidis]	476	1.20E-99
EF008-2	gi 1573330	adhesin B precursor (fimA) [Haemophilus influenzae]	380	1.60E-68
EF008-2	gi 1245464	YfeA [Yersinia pestis] >gi 1245464 YfeA [Yersinia pestis]	355	1.20E-64
EF008-2	gi 755075	periplasmic-binding protein [Synecocystis sp.] >gn PIDd1018652 Mn	321	1.70E-62
EF008-2	gi 1335912	EwIA [Erysipelothrix rhusiopathiae]	232	4.40E-42
EF008-2	gn PIIle118595	similar to ABC transporter (membrane protein) [Bacillus]	204	4.10E-38
EF008-2	gi 1777933	TroA [Treponema pallidum]	181	2.40E-35
EF009-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir N0752 N0752 outer	391	4.00E-64
EF009-2	gi 1552773	hypothetical [Escherichia coli] ~gn PIDd1012634 hypothetical 29.4	350	1.90E-63
EF009-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	391	6.40E-63
EF009-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir N0753 N0753 outer	386	1.10E-61
EF009-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	286	5.60E-60
EF009-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	286	7.60E-60
EF009-2	gi 294069	lipoprotein 1 [Pasteurella haemolytica]	122	4.70E-59
EF009-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	326	2.20E-58
EF009-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	239	7.80E-57
EF009-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	344	4.90E-56
EF009-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	319	4.20E-53
EF009-2	gi 2196096	lipoprotein homolog [Treponema pallidum] ~gi 2108234 29K protein	312	2.60E-51

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF009-2	gi 1336657	lipoprotein [Bacillus subtilis]	234	4.00E-32
EF009-2	gn PID e233873	hypothetical protein [Bacillus subtilis] >gn PID e1182900	242	1.40E-31
EF009-2	gn PID e118435	similar to hypothetical proteins [Bacillus subtilis]	102	6.80E-22
EF011-2	gn PID d10096 5	ferric anguibactin-binding protein precursor FatB of V.	579	3.10E-98
EF011-2	gn PID d10096 5	ferric anguibactin-binding protein precursor FatB of V.	579	3.10E-98
EF011-2	gn PID e185374	ccuE gene product [Campylobacter coli]	284	1.30E-89
EF011-2	gn PID e185374	ccuE gene product [Campylobacter coli]	284	1.30E-89
EF011-2	gi 150756	40 kDa protein [Plasmid pM1] >pirA29928 A29928 membrane-associated	232	2.80E-52
EF011-2	gi 150756	40 kDa protein [Plasmid pM1] >pirA29928 A29928 membrane-associated	232	2.80E-52
EF011-2	gi 309362	pheromone binding protein [Plasmid pC110] >pir B53309 B53309	366	8.30E-110
EF012-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	252	1.10E-109
EF012-2	gn PID d10118 5	TRAC [Enterococcus faecalis]	281	3.60E-103
EF012-2	gn PID d10065 5	Trac [Enterococcus faecalis]	277	2.50E-102
EF012-2	gi 12940	phosphorylase kinase [Streptococcus equi subsp. 1] >pir S28153 S28153	232	1.90E-67
EF012-2	gi 48808	dciAE [Bacillus subtilis]	228	1.70E-46

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF012-2	pir S16651 S166	dciAE protein - <i>Bacillus subtilis</i>	228	1.00E-45
EF012-2	gnl PID e118149	(AJ002571) DppE [<i>Bacillus subtilis</i>] >gnl PID e1183316	228	3.80E-45
EF012-2	gi 40005	OppA gene product [<i>Bacillus subtilis</i>]	281	3.90E-44
EF012-2	gi 143603	sporulation protein [<i>Bacillus subtilis</i>] >gnl PID e1183163	281	7.70E-44
EF012-2	gnl PID d10156 3	Periplasmic oligopeptide-binding protein precursor.	152	2.20E-43
EF012-2	gi 1574679	oligopeptide binding protein (oppA) [<i>Haemophilus influenzae</i>]	178	2.20E-42
EF012-2	gi 47802	Opp A (AA1-542) [<i>Salmonella typhimurium</i>] >gi 47808 precursor	128	1.00E-37
EF012-2	gi 882550	(ORF_1535 [<i>Escherichia coli</i>] >gi 1789397 (AF000384) 1535; This 535 aa	228	5.30E-36
EF014-2	pir D70070 D70 0	transcriptional regulator homolog yvfF - <i>Bacillus subtilis</i>	101	1.40E-27
EF014-2	gnl D70070 D70 0	transcriptional regulator homolog yvfF - <i>Bacillus subtilis</i>	121	9.30E-27
EF014-2	gi 2804769	(AF030373) putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	9.50E-27
EF014-2	gnl PID e289126	unknown [<i>Streptococcus pneumoniae</i>]	121	1.00E-24
EF014-2	gi 2267239	ORF1 [<i>Staphylococcus epidermidis</i>]	234	1.50E-24
EF014-2	gi 485275	putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	3.90E-24
EF014-2	gi 2804769	(AF030373) putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	3.90E-24
EF014-2	gi 2804769	(AF030373) putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	3.90E-24
EF014-2	gi 2804769	(AF030373) putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	3.90E-24

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF014-2	gjl1762327	putative transcriptional regulator [Bacillus subtilis]	185	2.80E-22
EF014-2	gjl143156	membrane bound protein [Bacillus subtilis] >gjlPIDle1184471	116	1.10E-21
EF014-2	gjlPID[d10189 5	membrane bound protein LytR [Synecocystis sp.]	113	6.20E-20
EF014-2	gjl1276874	EpsA [Streptococcus thermophilus]	103	4.00E-17
EF016-2	gjlPIDle118566	similar to amino acid ABC transporter (binding protein)	194	3.70E-35
EF016-2	gjl40934	arginine binding protein [Escherichia coli] >gjl769794 artJ	121	1.60E-31
EF016-2	gjlPID[d10152 7	Arginine-binding periplasmic protein 2 precursor [Escherichia coli]	121	4.80E-31
EF016-2	gjl687652	Arginine-binding periplasmic protein 2 precursor [Escherichia coli]	160	3.20E-31
EF016-2	gjl3650410	glutamine ABC transporter, periplasmic glutamine binding precursor [AE001090]	122	3.30E-29
EF016-2	gjl164663	glutamine-binding periplasmic protein (glnI) [Haemophilus influenzae]	174	2.50E-27
EF016-2	gjl1574634	GlnI precursor (AA -22 to 226) [Escherichia coli]	106	4.70E-27
EF016-2	gjl41569	>gjlPID[d1015250]	109	3.70E-26
EF016-2	gjlPID[d10152 7	Arginine-binding periplasmic protein 1 precursor [Escherichia coli]	117	8.50E-24
EF016-2	gjlPID[d10089 2	homologous to Gln-binding periplasmic proteins [Bacillus subtilis]	118	2.10E-23
EF016-2	gjl54125	J protein [Salmonella typhimurium] >gjl47718 reading frame	118	2.10E-23

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	hisJ			
EF016-2	gnl PID d10168 8	HISTIDINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (HBP).	117	4.50E-23
EF016-2	gi 1166636	histidine-binding periplasmic protein HisJ [Escherichia coli]	117	6.60E-23
EF017-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	421	4.50E-128
EF017-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	417	5.10E-124
EF017-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	414	4.40E-123
EF017-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	415	2.40E-119
EF017-2	gi 40005	OppA gene product [Bacillus subtilis]	294	6.20E-82
EF017-2	gi 43603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	290	2.80E-70
EF017-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	241	2.40E-71
EF017-2	gi 48808	dcfAE [Bacillus subtilis]	270	1.10E-61
EF017-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	270	1.50E-61
EF017-2	pir S16651 S166	dcfAE protein - Bacillus subtilis	270	3.10E-60
EF017-2	gi 304925	periplasmic oligopeptide binding protein [Escherichia coli]	171	2.60E-57
EF017-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	171	8.70E-56
EF017-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	154	1.30E-52

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF017-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa	135	5.50E-52
EF017-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	168	2.90E-43
EF019-2	gi 438458	likely N-terminal signal sequence; mature protein probably	104	2.30E-17
EF021-2	gn PID e311492	unknown [Bacillus subtilis] >gn PID e1184232 similar to ABC	317	2.50E-103
EF021-2	bbs 173803	CD44 T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167,	476	2.80E-81
EF021-2	gi 581809	trnC gene product [Treponema pallidum] - pitA43595A43595	152	3.20E-71
EF021-2	gi 2688280	membrane (AL001143) basic membrane protein C (bmpC) [Borrelia burgdorferi]	101	5.50E-27
EF021-2	gn PID e117283	membrane protein A [Borrelia garinii]	142	6.50E-22
EF021-2	gn PID e117283	membrane protein A [Borrelia burgdorferi]	141	9.20E-22
EF021-2	gn PID e117283	membrane protein A [Borrelia burgdorferi] - gp316592	141	9.30E-22
EF021-2	gn PID e117283	membrane		
EF021-2	gn PID e117283	bmpA(p39,ORF1) [Borrelia burgdorferi]	141	1.70E-21
EF021-2	gi 508421	antigen P39 [Borrelia burgdorferi] >gi 2688281 (AE001143) basic	141	1.70E-21
EF021-2	gi 1753225	BmpA protein [Borrelia burgdorferi]	141	2.70E-20
EF021-2	gn PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gn PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gn PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gn PID e117282	bmpA(p39,ORF1) [Borrelia burgdorferi]	141	1.50E-19

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF022-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	324	5.90E-66
EF022-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	307	5.60E-60
EF022-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	301	4.80E-59
EF022-2	gnl PID e118149	(A1002571) DppE [Bacillus subtilis] >gnl PID e1183316	170	5.10E-59
EF022-2	gi 48808	deiAE [Bacillus subtilis]	170	5.20E-59
EF022-2	gnl PID d10065 5	traC [Enterococcus faecalis]	299	2.80E-58
EF022-2	pir S16651 S166	deiAE protein - Bacillus subtilis	170	1.60E-57
EF022-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAMP binding	280	2.70E-53
EF022-2	gi 40005	OppA gene product [Bacillus subtilis]	154	7.30E-48
EF022-2	gi 43603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	154	3.10E-47
EF022-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	215	1.00E-36
EF022-2	gi 2281458	(AF000366) oligopeptide permease homolog Ali [Borrelia burgdorferi]	215	1.00E-36
EF022-2	gi 304025	periplasmic oligopeptide binding protein [Escherichia coli]	131	1.20E-35
EF022-2	gi 47014	oligopeptide binding protein precursor [Escherichia coli]	131	1.80E-34
EF022-2	gi 47802	OppA (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	138	4.90E-34
EF023-2	gi 309662	pheromone binding protein [Plasmid pCF10]	231	4.70E-66

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir B53309 B53309			
EF023-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	223		4.80E-62
EF023-2	gn PID d101185	TRAC [Enterococcus faecalis]	226		1.00E-58
EF023-2	gn PID d100655	TraC [Enterococcus faecalis]	226		4.40E-58
EF023-2	gi 48808	deiAE [Bacillus subtilis]	157		1.20E-57
EF023-2	gn PID c118149	[A1002571] DppE [Bacillus subtilis] - gi PID c1183316	157		1.20E-57
EF023-2	pir S16651 S166	deiAE protein - Bacillus subtilis	157		3.80E-56
EF023-2	gi 40005	OppA gene product [Bacillus subtilis]	137		2.30E-53
EF023-2	gi 43603	sporulation protein [Bacillus subtilis] - gi PID c11833163	133		6.90E-53
EF023-2	gi 47802	OppA (AA1-542) [Salmonella typhimurium] - gi 47808 precursor	133		2.00E-41
EF023-2	gi 2688227	(AF001139) oligopeptide ABC transporter, petriplasme	187		9.40E-41
EF023-2	gi 2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	187		1.90E-40
EF023-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AF000384) f535; This 535 aa	155		1.30E-38
EF023-2	gi 304923	periplasmic oligopeptide binding protein [Escherichia coli]	130		9.00E-37
EF023-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	130		3.20E-34
EF026-2	gi 2352482	(AF005097) unknown [Lactococcus lactis]	141		1.10E-23
EF027-2	gi 309662	pheromone binding protein [Plasmid pCl-10]	198		6.20E-71

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir B53309 B53309		
EF027-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	202	1.50E-68
EF027-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	202	1.50E-68
EF027-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	213	8.30E-68
EF027-2	gnl PID d118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID d1183316	222	3.70E-41
EF027-2	gi 48808	deiAE [Bacillus subtilis]	222	4.90E-41
EF027-2	pir S16651 S166	deiAE protein - Bacillus subtilis	222	1.10E-39
EF027-2	gi 40005	OppA gene product [Bacillus subtilis]	251	4.10E-39
EF027-2	gi 113603	sporulation protein [Bacillus subtilis] >gnl PID d1183163	247	5.80E-39
EF027-2	gi 312910	threonine kinase [Streptococcus equisimilis]	233	8.90E-33
		>pir S28153 S28153		
EF027-2	gi 2688227	(AF001139) oligopeptide ABC transporter, periplasmic	131	2.40E-24
EF027-2	gi 2281458	(AF000366) oligopeptide permease homolog All [Borrelia burgdorferi]	131	2.40E-24
EF027-2	gi 2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AF000792)	117	3.00E-20
EF027-2	gi 1336079	oligopeptide binding protein (oppA) [Haemophilus influenzae]	130	3.50E-20
EF028-2	gnl P13110204 7	B. subtilis alkaline phosphatase IIIA; P19403 secondary	996	3.60E-131
EF028-2	pir B39099 B39	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus	982	2.90E-129

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF029-2	gi 47146	thermonuclease [Staphylococcus intermedius] >pir S26079 S26079	145	4.90E-32
EF030-2	gi 48808	dciAE [Bacillus subtilis]	149	1.10E-66
EF030-2	gn PID e118149	(AJ002571) DppE [Bacillus subtilis] >gn PID e1183316	149	1.50E-66
EF030-2	pir S16651 S166	dciAE protein - Bacillus subtilis	149	5.90E-66
EF030-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	227	7.40E-52
EF030-2	gn PID d10118	TRAC [Enterococcus faecalis]	237	7.40E-52
EF030-2	5	TrnC [Enterococcus faecalis]	233	9.70E-51
EF030-2	gn PID d10065	5	229	3.00E-48
EF030-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	277	3.00E-45
EF030-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	125	8.50E-34
EF030-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	211	4.80E-31
EF030-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	211	4.80E-31
EF030-2	gi 2281458	(AF009566) oligopeptide permease homologue AII [Borrelia burgdorferi]	148	1.20E-30
EF030-2	gi 10005	OppA gene product [Bacillus subtilis]	144	4.80E-30
EF030-2	gi 143603	sporulation protein [Bacillus subtilis] >gn PID e1183163	210	2.10E-29
EF030-2	gi 2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AE000792)		

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF030-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	148	6.00E-29
EF033-2	gn PID e118439	similar to iron-binding protein [Bacillus subtilis]	164	2.60E-14
EF033-2	pir S54437 S544	hemin binding protein - Yersinia enterocolitica	108	1.40E-11
EF033-2	gi 1619623	hemin binding protein [Yersinia enterocolitica]	108	2.00E-11
EF036-2	gn PID d10102 2	ORF108 [Bacillus subtilis] >gn PID e1185766 alternate gene	544	1.20E-96
EF036-2	gi 26222858	(AE000929) phosphate-binding protein PstS [Methanobacterium]	183	1.40E-45
EF036-2	gi 26222858	(AF000929) phosphate-binding protein PstS homolog [Methanobacterium]	178	2.40E-41
EF036-2	gi 2688115	(AE001132) phosphate ABC transporter, periplasmic phosphate-binding	117	1.10E-12
EF037-2	gi 2352482	(AF005097) unknown [Lactococcus lactis]	141	1.10E-23
EF040-2	gi 1657516	hypothetical protein [Escherichia coli] >gi 186511 AF000139	208	1.90E-29
EF040-2	gi 293265	2-5A-dependent RNase [Mus musculus] >pir B45771 B45771	105	1.00E-17
EF040-2	gi 287865	G9a [Homo sapiens] >pir S30385 S30385 G9a protein - human	143	8.30E-14
EF040-2	gi 311817	erythroid ankyrin [Mus musculus] >pir S37771 S37771 ankyrin,	119	4.80E-13
EF040-2	gi 191940	ankyrin [Mus musculus] >pir 49502 49502 ankyrin - mouse	119	4.90E-13
EF040-2	gi 247710	alt. ankyrin (variant 2.2) [Homo sapiens]	120	1.50E-12
EF040-2	gi 178946	ankyrin [Homo sapiens]	120	1.60E-12
EF040-2	gi 1845265	ankyrin [Homo sapiens]	120	1.80E-12
EF040-2	pir A35049 A350	ankyrin 1, erythrocyte splice form 2 - human	120	1.80E-12
	0			

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF040-2	pir B35049 B350	ankyrin 1, erythrocyte splice form 3 - human	120	1.80E-12
EF040-2	gi 28702	ankyrin (variant 2.1) [Homo sapiens] >pir S08275 SJHUK	120	1.80E-12
EF041-2	gi 388269	ankyrin 1, traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	670	1.40E-87
EF041-2	gnl PID d1100655	TraC [Enterococcus faecalis]	662	1.50E-85
EF041-2	gnl PID d1101185	TRAC [Enterococcus faecalis]	662	1.50E-85
EF041-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	648	1.20E-83
EF041-2	gi 48808	dciAE [Bacillus subtilis]	218	1.20E-57
EF041-2	gnl PID e118149	(A1002571) DppE [Bacillus subtilis] >gnl PID e1183316	218	1.40E-57
EF041-2	pir S16651 S166	dciAE protein - Bacillus subtilis	218	2.10E-56
EF041-2	gi 882550	ORF_1535 [Escherichia coli] >gi 1789397 (AF000384) 1535; This 535 aa	146	7.30E-40
EF041-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	278	1.00E-34
EF041-2	gi 40005	OppA gene product [Bacillus subtilis]	279	1.00E-34
EF041-2	gi 34342	OppA (A1452) [Salmonella typhimurium] >gi 17508 precursor	141	6.60E-30
EF041-2	gi 36425	periplasmic oligopeptide binding protein [Escherichia coli]	160	1.90E-29
EF041-2	gi 574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	163	1.00E-28

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF049-2	gi 472835	ORF1 [Lactococcus lactis cremoris]	241	1.50E-53
EF049-2	gi 39782	33kDa lipoprotein [Bacillus subtilis] >gnl PID e325181 33kDa	128	8.90E-40
EF051-2	gnl PID d10114 2	molybdate-binding periplasmic protein [Synechocystis sp.]	173	3.20E-50
EF051-2	gnl PID e118602	alternate gene name: yvsD; similar to molybdate-binding	314	5.90E-50
EF051-2	gi 1574546	lsg locus hypothetical [Haemophilus influenzae] >pir A64175 A64175	161	2.20E-43
EF051-2	gi 504498	periplasmic molybdate-binding protein [Escherichia coli] >gi 1147817	148	1.40E-30
EF051-2	gi 148939	ORF 8 [Haemophilus influenzae] >pir S27583 S27583 hypothetical	150	8.10E-28
EF054-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	1490	1.80E-192
EF054-2	gnl PID e236571	cell wall anchoring signal [Enterococcus faecalis]	515	8.10E-64
EF054-2	gi 45738	ORF-C [Enterococcus faecalis] >pir H10204 H10204 hypothetical 30.5K	372	1.60E-58
EF054-2	gi 496520	orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical	362	1.30E-43
EF054-2	gi 160693	sporozoite surface protein [Plasmodium yoelii] >pir A45559 A45559	286	4.30E-33
EF054-2	gi 160693	hypothetical [Plasmodium yoelii]	305	1.30E-32
EF054-2	gi 160693	hypothetical protein [Bacillus subtilis] >gnl H10204 H10204	216	3.00E-26
EF051-2	gi 2200391	IgG and IgE immunoreactive antigen recognized by sera from patients	242	1.40E-25

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF054-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25
EF054-2	gi 46523	B antigen [Streptococcus agalactiae]	232	2.80E-23
EF054-2	pir S15330 FCS O	IgA Fc receptor precursor - Streptococcus agalactiae	228	1.00E-22
EF054-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	210	3.10E-21
EF054-2	gi 63686	NF-M c-terminus [Gallus gallus]	222	6.90E-21
EF054-2	gi 63689	NF-M protein [Gallus gallus] >pir S15762 S15762 neurofilament triplet	222	8.50E-21
EF054-2	gi 757867	TATA-box like sequence (Us11) [Human herpesvirus 1] >gi 291493 18	194	4.10E-19
EF059-2	gi 1110236571	cell wall anchoring signal [Enterococcus faecalis]	418	5.60E-95
EF059-2	gi 150556	surface protein [Phage phiCF10] >pir A41826 A41826 probable	606	3.70E-87
EF059-2	gi 45738	ORF3 [Enterococcus faecalis] >pir H10204 H10204 hypothetical 30.5K	366	9.30E-50
EF059-2	gi 496520	orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical	367	5.90E-44
EF059-2	gi 160693	sporozoite surface protein [Plasmodium voelii] >pir A45501 A45501	344	1.10E-38
EF059-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25
EF059-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF059-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	253	6.40E-27
EF059-2	gi 46521	Fc receptor [Streptococcus agalactiae] >pir A60234 A60234 IgA	197	2.70E-26
EF059-2		Fc		
EF059-2	gi 46523	B antigen [Streptococcus agalactiae]	232	9.30E-26
EF059-2	pir S15330 FCS	IgA Fc receptor precursor - Streptococcus agalactiae	232	9.30E-26
EF059-2	O			
EF059-2	gnl PID e225687	zinc finger protein [Mus musculus] >gnl PID e225688 zinc	234	1.40E-22
EF059-2	gi 423356	zona pellucida protein [Pseudopleuronectes americanus]	229	1.00E-21
EF059-2	gi 457769	Collagen [Bombyx mori] >pir S42886 S42886 collagen -	209	7.60E-19
EF059-2		silkworm		
EF061-2	gnl PID e236571	cell wall anchoring signal [Enterococcus faecalis]	925	8.10E-118
EF061-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	350	1.50E-107
EF061-2	gi 406520	orf104 [Streptococcus pyogenes] >pir S68125 S45091	308	1.40E-58
EF061-2		hypothetical		
EF061-2	gi 45738	ORF3 [Enterococcus faecalis] >pir H0204 H0204	322	6.40E-50
EF061-2		hypothetical 30.5K		
EF061-2	gi 1813523	PbTRAP [Plasmodium berghei]	263	1.00E-26
EF061-2	gi 160693	sporozoite surface protein [Plasmodium yoelii]	241	9.00E-25
EF061-2		sp A45550 A45559		
EF061-2		hypothetical 30.5K		
EF061-2	gi 160693	sporozoite surface protein [Plasmodium yoelii]		
EF061-2		neurofilament triplet		
EF061-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from	176	2.40E-21

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		patients			
EF061-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	165	2.70E-20	
EF061-2	gn PID e225687	zinc finger protein [Mus musculus] >gn PID e225688 zinc	197	7.80E-19	
EF061-2	gi 160355	interspersed repeat antigen [Plasmodium falciparum]	199	8.20E-18	
EF061-2	gi 410750	interspersed repeat antigen [Plasmodium falciparum]	199	8.90E-18	
EF061-2	gi 2290388	IgG and IgE immunoreactive antigen recognized by sera from patients	182	1.40E-17	
EF061-2	gi 2290394	IgG and IgE immunoreactive antigen recognized by sera from patients	180	2.80E-17	
EF062-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0	
EF062-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0	
EF062-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0	
EF062-2	gi 150555	aggregation substance [Plasmodium falciparum] pif 11662 H11662	6338	0	
EF062-2	gi 1109773	150K mating	110	9.90E-39	
EF062-2	gi 47248	SSPB precursor [Streptococcus gordonii]	107	1.70E-38	
EF062-2	gn PID 10150	PAC protein precursor (AA -38 to 1527) [Streptococcus mutans]	132	5.00E-36	
EF062-2	gi 149433	surface protein antigen precursor [Streptococcus sobrinus]	132	1.20E-38	

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF062-2	gi 47620	antigen I/II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF062-2	pir A35186 A351	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34
EF062-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF062-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF063-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF063-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0
EF063-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF063-2	gi 150555	aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating	6338	0
EF063-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF063-2	gi 17248	PAC protein precursor (AA 38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF063-2	gn P1D6d101507	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF063-2	gi 47267	cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839	107	6.50E-36
EF063-2	bbs 18153	SspA endocarditis immunodominant antigen [Streptococcus	132	1.20E-35
EF063-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF063-2	pir A35186 A351	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF063-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF063-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF064-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF064-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0
EF064-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF064-2	gi 150555	aggregation substance [Plasmid pC1-10] >pir H41662 H41662 150K mating	6338	0
EF064-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF064-2	gi 47248	PAc protein precursor (AA -38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF064-2	gn PID d10150 7	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF064-2	gi 152267	cell surface antigen I II [Streptococcus mutans] >pir S06839 S06839	107	6.20E-36
EF064-2	gb 148153	SspA endocarditis immunodominant antigen [Streptococcus sobrinus,	132	1.20E-35
EF064-2	gi 47620	antigen I/II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF064-2	gi 1533843	cell surface protein precursor [Streptococcus mutans]	107	5.10E-34
EF064-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF068-2	gi 790398	T061D8.1 [Caenorhabditis elegans]	137	8.50E-17

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF068-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF068-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF068-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF068-2	gi 1707247	partial CDS [Caenorhabditis elegans]	131	3.70E-15
EF068-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203	6.20E-15
EF068-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps] >pir A38420 A38420	102	4.60E-13
EF068-2	gnl PID c125164	(AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF068-2	gi 29051460	HM C-1 gene product [Xenopus laevis] >pir A45155 A45155	109	2.70E-12
EF069-2	gi 790398	mucin T061D8.1 [Caenorhabditis elegans]	137	8.50E-17
EF069-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF069-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF069-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF069-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203	6.20E-15
EF069-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps]	102	4.60E-13

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF069-2	gnl PID e125464	>pir A38420 A38420 (AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF069-2	gil951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 mucin	109	2.70E-12
EF070-2	gil700398	T06108.1 [Caenorhabditis elegans]	137	8.50E-17
EF070-2	gnl PID d102084	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF070-2	gil2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF070-2	gil330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF070-2	gil1707247	partial CDS [Caenorhabditis elegans]	131	3.70E-15
EF070-2	gil33918d102084	membrane glycoprotein [Equine herpesvirus 1]	303	1.60E-15
EF070-2	gil213392	antifreeze glycoprotein [Notothenia cornueps]	102	4.60E-15
EF070-2	gnl PID e125464	>pir A38420 A38420 (AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF070-2	gil951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155	109	2.70E-12
EF071-2	gil853751	Lysyl	273	2.60E-36
EF073-2	gil143830	N-acetylhistidine, L-L-alanine amidase [Pseudomonas AS11] xpaC [Bacillus subtilis] >gnl PID d1005803 hydrolysis of	173	7.10E-16

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF077-2	gij150719	cadmium resistance protein [Plasmid pI258] >pir A32561 A32561	373	8.60E-112
EF077-2	gij143753	cadmium-efflux ATPase [Bacillus firmus] >pir D42707 D42707 probable	361	8.10E-111
EF077-2	gij152978	Fe1-Fe2 cadmium efflux adenosine triphosphatase [Staphylococcus]	381	4.30E-110
EF077-2	gnl PIDe248808	unknown [Mycobacterium tuberculosis]	298	3.50E-107
EF077-2	gij495646	ATPase [Transposon Tn5422]	361	2.10E-106
EF077-2	gnl PIDe118497	similar to heavy metal-transporting ATPase [Bacillus]	286	3.50E-104
EF077-2	gij1699049	cadmium resistance protein [Lactococcus lactis]	352	3.60E-100
EF077-2	gnl PIDe118603	similar to heavy metal-transporting ATPase [Bacillus]	254	9.90E-100
EF077-2	gnl PIDe306540	unknown [Mycobacterium tuberculosis]	352	5.20E-88
EF077-2	gnl PIDe26333	Fe-type ATPase [Mycobacterium tuberculosis]	199	3.70E-86
EF077-2		>gnl PIDe249413		
EF077-2	gnl PIDe264090	unknown [Mycobacterium tuberculosis]	250	3.00E-84
EF077-2	gnl PIDd10113 5	cadmium-transporting ATPase [Synechocystis sp.]	260	1.00E-81
EF077-2	gij1773166	probable copper-transporting atpase [Escherichia coli] >gij1773166	212	4.70E-80
EF077-2	gij14911	probable copper-transporting atpase [Escherichia coli] >gij14911		
EF077-2	gij14911	probable copper-transporting atpase [Escherichia coli] sensor	212	4.70E-80

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF078-2	gnl PID d10119 6	homologous to sp:PHOR_BACSU [Bacillus subtilis]	219	4.20E-44
EF078-2	gil1575578	histidine protein kinase [Thermotoga maritima]	191	7.10E-44
EF078-2	gil2182990	histidine kinase [Lactococcus lactis cremoris]	169	6.40E-40
EF078-2	gil2182992	histidine kinase [Lactococcus lactis cremoris]	152	1.10E-39
EF078-2	gnl PID d10113 4	sensory transduction histidine kinase [Synechocystis sp.]	259	3.90E-38
EF078-2	gil149296	phosphate regulatory protein phoR (gtg start codon) [Klebsiella]	228	7.60E-33
EF078-2	gil581188	phoR gene product (AA 1-431) [Escherichia coli] >gil1657596	226	1.60E-32
EF078-2	gnl PID d10108 7	sensory transduction histidine kinase [Synechocystis sp.]	138	3.70E-32
EF078-2	gnl PID c266592	unknown [Mycobacterium tuberculosis]	232	1.10E-31
EF078-2	gil2182996	histidine kinase [Lactococcus lactis cremoris]	205	1.30E-31
EF078-2	gnl PID d10113 5	sensory transduction histidine kinase [Synechocystis sp.]	256	1.30E-31
EF078-2	gil294893	phosphate regulatory protein phoR (gtg start codon) [Shigella]	225	1.60E-31
EF078-2	gil288420	drug sensory protein A [Synechocystis PCC6803] >gnl PID d1017420	106	2.50E-31
EF078-2	gil2908210	putative fibronectin-associated protein [Actinomyces naeslundii] [Actinomyces naeslundii] >gil2908210	183	8.60E-26
EF081-2	gil790433	low affinity penicillin-binding protein 5 (PBPS) [Enterococcus]	604	2.70E-78

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF081-2	gi 790437	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus]	602	5.10E-78
EF081-2	gi 790431	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus]	591	2.60E-77
EF081-2	gi 43342	D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae]	587	9.30E-77
EF081-2	gi 49000	D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae]	572	5.20E-74
EF081-2	gnl PID d10079	penicillin-binding protein 2 [Bacillus subtilis]	149	7.40E-24
EF081-2	4			
EF081-2	gnl PID e315088	MecA1 [Staphylococcus sciuri]	111	1.40E-19
EF081-2	gnl PID e286651	MecA protein [Staphylococcus sciuri]	106	2.90E-18
EF081-2	gnl PID e316581	MecA protein [Staphylococcus sciuri]	111	2.90E-18
EF081-2	gnl PID e316607	MecA2 protein [Staphylococcus sciuri]	101	3.70E-14
EF081-2	gnl PID e316613	MecA protein [Staphylococcus sciuri] - gi 46613 mecA gene	101	3.70E-14
EF083-2	gi 496283	lysM [Bacteriophage Tuc2009]	436	6.20E-176
EF083-2	gi 530798	LysB [Bacteriophage phi-LC3]	421	5.00E-175
EF083-2	gi 166183	muramidase [Bacteriophage CP-7]	186	1.20E-21
EF083-2	gi 166188	muramidase [Bacteriophage CP-9] - put JQ0438 MUBPC9	188	5.00E-21
EF083-2	gi 623084	muramidase; muramidase [Bacteriophage LL-H]	193	8.40E-20
EF083-2	gi 166175	muramidase [Bacteriophage CP-1]	175	3.40E-19
EF083-2	gnl PID e221272	lysM gene [Bacteriophage CP-1] - put JQ0438 MUBPC9	174	3.40E-19
EF083-2		lysA -		
EF083-2	gi 793850	lysM [Lactobacillus bacteriophage phi adh] - gnl PID e1217314	117	5.60E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		lysine		438	1.70E-140
EF084-2	gi 2293312	(AF008220) YtfP [Bacillus subtilis] >gnl PID e 1185879 similar to			
EF084-2	gi 2367234	(AF000425) hypothetical 43.8 kD protein in rhsB-pit intergenic	167		2.20E-51
EF084-2	gi 912464	No definition line found [Escherichia coli]	167		6.00E-51
EF084-2	gnl PID d 101127	hypothetical protein [Synecococcus sp.] >pir S76678 S76678	151		6.10E-42
EF084-2	gi 1573954	hypothetical [Haemophilus influenzae] >pir G64161 G64161	142		2.90E-40
EF085-2	gi 1209527	protein histidine kinase [Enterococcus faecalis]	2023		8.00E-279
EF085-2	gi 467057	phoR; B2168_C3_247 [Mycobacterium leprae] >pir S72905 S72905	226		8.80E-23
EF085-2	gnl PID e 119229	SenX3 [Mycobacterium bovis BCG]	222		3.10E-22
EF085-2	gnl PID e 251152	unknown [Mycobacterium tuberculosis] >gnl PID e 321546	222		3.10E-22
EF085-2	gi 1778485	SenX3			
EF085-2		PcoS homolog [Escherichia coli] >gi 1786783 (AE000162) f480; This	111		3.80E-16
EF085-2	gi 149296	phosphate regulatory protein phoR (gtg start codon) [Klebsiella]	110		1.40E-14
EF085-2	gi 581188	phoR gene product (AA 1-431) [Escherichia coli] >gi 1657596	103		5.30E-14
EF085-2		base in			
EF085-2	gi 2182972	histidine kinase [Lactococcus lactis cremoris]	109		5.90E-12

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF086-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF086-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF086-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] [pir A55137 A55137]	203	3.30E-44
EF086-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	194	3.40E-42
EF086-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF087-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF087-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF087-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] [pir A55137 A55137]	203	3.30E-44
EF087-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	194	3.40E-42
EF087-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF088-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF088-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF088-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae]	203	3.30E-44
EF091-2	gi 566016	similar to plant water stress protein 3.02F1 [Vaccinium adami]	198	5.50E-21
EF091-2	gi 2353333	(AF016513) Ce-LEA [Caenorhabditis elegans]	189	2.40E-17

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF091-2	gn PID e353216	seed maturation protein homolog [<i>Arabidopsis thaliana</i>]	146	3.60E-11
EF091-2	gi 1161171	late embryogenesis abundant protein [<i>Picea glauca</i>]	132	5.70E-11
EF091-2	pir S04909 S049	embryonic protein DC8 (clone 8/10) - carrot	127	6.50E-11
EF092-2	gi 2689898	(AE000792) PTS system, cellobiose-specific IIB component (celA)	145	4.00E-27
EF092-2	gn pir 0419204	<i>B. subtilis</i> , cellobiose phosphorylase system celA;	116	1.40E-26
EF096-2	gi 147329	transport protein [<i>Escherichia coli</i>] >gn PID d1015409	532	2.10E-91
EF096-2	gi 1573475	spermidine/putrescine-binding periplasmic protein precursor (potD)	527	1.10E-79
EF096-2	gi 1574803	spermidine/putrescine-binding periplasmic protein precursor (potD)	468	1.60E-75
EF096-2	gi 1472681	Lpp38 [<i>Pasteurella haemolytica</i>]	446	1.40E-72
EF096-2	gn PID d10152	Putrescine transport protein PotF [<i>Escherichia coli</i>]	216	1.50E-54
EF096-2	gi 147334	periplasmic putrescine binding protein [<i>Escherichia coli</i>]	216	2.10E-53
EF096-2	gi 2688565	(AE001165) spermidine/putrescine ABC transporter, PotD [<i>Salmonella typhimurium</i>]	240	2.00E-48
EF096-2	gi 1881733	PotD [<i>Salmonella typhimurium</i>]	253	2.70E-28
EF096-2	gi 1472681	Lpp38 [<i>Pasteurella haemolytica</i>]	446	1.40E-72
EF097-2	gi 42991	mannitol transport protein [<i>Bacillus stearothermophilus</i>]	547	4.90E-93
EF097-2	gi 42034	mannitol permease [<i>Escherichia coli</i>] >gi 46677 mannitol-	535	5.50E-85

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		specific		
EF097-2	gi 633650	enzyme II(mannitol) [Staphylococcus carnosus] >pir S68193 S22385	516	2.10E-82
EF097-2	gi 882462	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia	509	3.00E-76
EF097-2	gi 312763	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia	357	2.50E-70
EF097-2	gnl PID d10096 6	homologue of mannitol transport protein of B	492	3.10E-63
EF097-2	gnl PID d10079 2	mannitol-specific phosphotransferase enzyme II [Bacillus	484	5.20E-64
EF097-2	gi 1673855	(A1:000020) Mycoplasma pneumoniae, PIS system mannitol- specific	232	3.50E-59
EF097-2	gnl PID d10065 1	phosphotransferase enzymell, mannitol-specific [Mycoplasma	158	8.20E-18
EF097-2	pir S77757 S777	phosphotransferase system enzyme II (EC 2.7.1.69),	103	2.00E-13
EF100-2	gi 2058546	ComYC [Streptococcus gordonii]	193	7.30E-27
EF100-2	gi 2058546	ComYC [Streptococcus gordonii]	193	7.30E-27
EF100-2	gi 127408	com63 gene product [Bacillus subtilis] (AF05739)	156	3.90E-33
EF100-2	gi 148437	secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic	134	4.40E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF100-2	gi 148437	secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic	134	4.40E-15
EF100-2	gi 606262	ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli]	136	9.10E-13
EF100-2	gi 606262	ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli]	136	9.10E-13
EF100-2	gi 38828	ExeG gene product [Acromonas hydrophila] >pir S22910 49905 protein	132	3.50E-12
EF100-2	gi 38828	ExeG gene product [Acromonas hydrophila] >pir S22910 49905 protein	132	3.50E-12
EF100-2	gn PID e117259	etpG [Escherichia coli]	131	5.10E-12
EF100-2	gn PID e117259	etpG [Escherichia coli]	131	5.10E-12
EF100-2	gi 42189	outG gene product [Erwinia carotovora] >pir S32861 S32861 outG	130	9.90E-12
EF100-2	gi 42189	outG gene product [Erwinia carotovora] >pir S32861 S32861 outG	130	9.90E-12
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF101-2	gn PID e118502	similar to hypothetical proteins from B. subtilis [Bacillus]	113	1.89E-15
EF110-2	gi 43538	Staphylococcal serine proteinase homologue [Enterococcus faecalis]	1462	2.30E-195

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EF110-2	gnl PID d10010 8	glutamic acid specific protease prepropeptide [Staphylococcus aureus]	106	3.70E-14
EF110-2	gi 46687	preproenzyme (AA -68 to 268) [Staphylococcus aureus]	106	6.70E-14
EF111-2	gi 606018	ORF_0783 [Escherichia coli] >gi 1789462 (AF000390) hypothetical_88.3	477	8.10E-80
EF121-2	gi 2626826	YtkN [Bacillus subtilis] >gnl PID d1182774 similar to (AF000532) 2',3'-cyclic nucleotide 2'-phosphodiesterase (cpdB)	143	1.30E-96
EF121-2	gi 2313187	(AF000532) 2',3'-cyclic nucleotide 2'-phosphodiesterase (cpdB)	413	2.60E-82
EF121-2	gi 48453	5' nucleotidase [Vibrio parahaemolyticus] >gnl PID d1001218	279	8.50E-47
EF121-2	gi 757842	UDP-sugar hydrolase [Escherichia coli]	239	1.60E-44
EF121-2	gi 1773162	UDP-sugar hydrolase precursor [Escherichia coli] >gi 1786687	239	1.60E-44
EF121-2	gi 47950	precursor polypeptide (AA -25 to 525) [Salmonella typhimurium]	229	2.10E-41
EF121-2	gi 747913	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia enterocolitica]	115	4.70E-36
EF121-2	gi 62772	5'-nucleotidase [Discopyge ommata] >pir S19564 S19564 5'- nucleotidase	137	5.80E-35
EF121-2	gi 1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus influenzae]	114	8.90E-34
EF121-2	gi 537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli]	110	1.10E-31
EF121-2	gi 203771	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Yersinia enterocolitica]	133	9.10E-28
EF121-2	gi 319783	ecto-5'-nucleotidase [Mus musculus] >pir C2001 C2001	136	1.10E-27

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF121-2	gi 23897	5'-nucleotidase [<i>Homo sapiens</i>] >pir S11032 S11032 5'-nucleotidase (EC)	133	1.60E-27
EF122-2	gi 2626826	YfkN [<i>Bacillus subtilis</i>] >gnl PID e1182774 similar to	143	1.30E-96
EF122-2	gi 2313187	(AE000532) 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)	413	2.60E-82
EF122-2	gi 38453	5'-nucleotidase [<i>Vibrio parahaemolyticus</i>] >gnl PID d1001218	279	8.50E-47
EF122-2	gi 757842	UDP-sugar hydrolase [<i>Escherichia coli</i>]	239	1.60E-44
EF122-2	gi 1773162	UDP-sugar hydrolase precursor [<i>Escherichia coli</i>] >gi 1786687	239	1.60E-44
EF122-2	gi 47950	precursor polypeptide (AA -25 to 525) [<i>Salmonella typhimurium</i>]	229	2.10E-41
EF122-2	gi 747913	2',3'-cyclic-nucleotide 2'-phosphodiesterase [<i>Yersinia</i>]	115	4.70E-36
EF122-2	gi 62772	5'-nucleotidase [<i>Discopyge ommata</i>] >pir S19564 S19564 5'-nucleotidase	137	5.80E-35
EF122-2	gi 1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [<i>Haemophilus</i>]	114	8.90E-34
EF122-2	gi 537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [<i>Escherichia coli</i>]	110	1.10E-31
EF122-2	bbs 135915	5'-nucleotidase=glycosylphosphatidylinositol-anchored protein {EC}	128	7.70E-29
EF122-2	gi 1737443	5'-nucleotidase [<i>Boophilus microplus</i>]	104	1.60E-28
EF122-2	gi 35354	5'-nucleotidase [<i>Enterococcus faecium</i>] >pir 305542 305542	630	9.40E-79

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		hypothetical		
EF129-2	gi 512521	usp 45 gene product [Lactococcus lactis] >pir JN0097 JN0097 secreted	374	1.30E-42
EF129-2	gi 149525	secreted protein [Lactococcus lactis]	371	3.60E-42
EF129-2	gn PID e313022	hypothetical protein [Bacillus subtilis] >gn PID e1186168	317	2.30E-33
EF130-2	gi 488339	alpha-amylase [unidentified cloning vector]	621	6.70E-81
EF130-2	gi 488336	ORF [unidentified cloning vector]	242	8.00E-27
EF130-2	bbs 112518	alpha-amylase {N-terminal region} [Artificial sequence, Peptide]	237	4.80E-26
EF130-2	gn PID e289144	ywpE [Bacillus subtilis] >gn PID e1184540 ywpE [Bacillus]	129	5.40E-11
EF131-2	gn PID e118528	penicillin-binding protein [Bacillus subtilis]	277	7.40E-43
EF131-2	gi 488330	alpha-amylase [unidentified cloning vector]	280	1.30E-31
EF131-2	gi 509240	No definition line found [Lactobacillus plantarum]	274	1.10E-30
EF131-2	gn PID d10249	(AB009635) Fmt [Staphylococcus aureus]	170	5.60E-20
EF131-2	gi 515050	DD-peptidase precursor [Streptomyces lividans] >pir S48220 S48220	131	2.30E-14
EF131-2	gi 153448	serine DD-peptidase [Streptomyces lividans]	131	1.20E-12
EF132-2	gi 153876	adhesin B [Streptococcus subtilis] >pir S48220 S48220	1220	3.70E-166
EF132-2	gi 203360	adhesin protein [Streptococcus pneumoniae]	1301	3.40E-163
EF132-2	gi 1575030	surface adhesin A precursor [Streptococcus pneumoniae]	1220	2.40E-161

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF132-2	gi 153834	adhesin specific for salivary pellicle of dental surfaces	1203	4.80E-159
EF132-2	gi 1117994	surface antigen A variant precursor [Streptococcus pneumoniae]	1191	2.00E-157
EF132-2	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	931	3.70E-122
EF132-2	gn PID c255529	lipoprotein [Staphylococcus epidermidis]	453	3.20E-92
EF132-2	gi 1215161	YfeA [Yersinia pestis] > gi 1245464 YfeA [Yersinia pestis]	364	3.60E-64
EF132-2	gi 1573330	adhesin B precursor (fimA) [Haemophilus influenzae]	349	3.50E-63
EF132-2	gi 755075	periplasmic-binding protein [Synecchocystis sp.]	326	6.80E-62
EF132-2	gn PID d1018652 Mn	similar to ABC transporter (membrane protein) [Bacillus]	174	3.10E-32
EF132-2	gi 1777933	TroA [Treponema pallidum]	171	3.40E-32
EF132-2	gi 790546	Tromp1 [Treponema pallidum]	171	5.10E-32
Query	Derwent Access. No.	Derwent Gene Description	BLAST Score	BLAST P-Value
EF003-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	268	4.20E-39
EF003-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	241	3.00E-27
EF006-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	283	1.20E-48
EF006-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	266	1.10E-30
EF009-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	319	1.40E-53

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF009-2	W20166	<i>Helicobacter pylori</i> outer membrane protein, 16225006.aa.	278	2.50E-32
EF012-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	227	3.20E-69
EF014-2	W14070	<i>S.thermophilus</i> exopolysaccharide biosynthesis protein EpsR.	103	5.90E-19
EF014-2	W22169	<i>S.thermophilus</i> exopolysaccharide synthesis operon epsA gene product.	103	7.30E-18
EF016-2	W15799	Adherence factor 104R of <i>Lactobacillus fermentum</i> .	157	9.60E-22
EF016-2	W15793	Adherence factor consensus sequence.	103	1.00E-11
EF017-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	241	8.90E-71
EF021-2	R31013	P39-alpha.	141	1.60E-19
EF021-2	R33280	P39-beta.	134	7.00E-14
EF022-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	324	2.20E-65
EF023-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	155	9.90E-33
EF023-2	R70152	<i>Streptococcus pneumoniae</i> strain SPR198 P1pA	125	5.90E-17
EF027-2	R48035	Hyaluronic acid synthase of <i>Streptococcus equisimilis</i> .	233	2.20E-34
EF028-2	W17830	Thermophilic alkaline phosphatase.	202	7.70E-59
EF028-2	W11568	<i>E.coli</i> alkaline phosphatase mutant D153H/Q329A.	182	7.90E-56
EF028-2	W11570	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q329A	182	7.90E-56
EF029-2	W26309	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q329A/P330H	182	7.90E-56
EF030-2	W11564	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q329A	182	7.90E-56
EF030-2	W11553	<i>E.coli</i> alkaline phosphatase mutant D153H/K328H/Q330N	182	7.90E-55

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF028-2	W11566	E.coli alkaline phosphatase mutant D153H/K328H/D330L.	182	1.20E-54
EF028-2	W11569	E.coli alkaline phosphatase mutant K328H/Q329A.	180	1.70E-54
EF028-2	W11562	E.coli alkaline phosphatase mutant D153H/D330L.	182	1.70E-54
EF028-2	R26980	Fv(FRP5)-phoA recombinant antibody.	174	1.90E-54
EF028-2	W11567	E.coli alkaline phosphatase mutant Q329A.	179	2.30E-54
EF028-2	W11558	E.coli alkaline phosphatase mutant K328H/D330N.	176	6.40E-54
EF028-2	W11563	E.coli alkaline phosphatase mutant K328H/D330A.	176	6.40E-54
EF029-2	R10044	plasmid pOW360 encoded Human Growth Hormone (HGH) - nuclease A	320	3.50E-40
EF029-2	R10041	Plasmid pOW350 nuclease A product.	320	4.30E-40
EF029-2	R73997	Staphylococcus aureus (Foggi) nuclease signal and mature sequences.	320	5.60E-40
EF029-2	R10043	Plasmid pOW360 encoding Human Growth Hormone (HGH) - nuclease	320	2.90E-38
EF030-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	277	6.10E-47
EF040-2	R59077	2-5A-dependent RNA-ase.	105	1.90E-18
EF040-2	W12703	Mouse 2-5A-dependent RNase.	105	1.90E-18
EF040-2	R82661	Partial murine 2-5A dependent RNase	105	1.90E-18
EF040-2	R48035	Partial murine 2-5A dependent RNase	225	6.30E-20
EF051-2	R85781	Group B Streptococcal wild-type beta antigen	232	5.20E-24

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF054-2	P91941	Sequence of preprospasmolysin.	204	3.10E-19
EF054-2	W32519	Collagen-like polypeptide SEQ ID NO:2.	180	7.50E-18
EF054-2	W12324	Silver halide emulsion protein monomeric repeat unit #2.	180	7.50E-18
EF054-2	W32522	Collagen-like polypeptide SEQ ID NO:5.	192	1.60E-17
EF054-2	W12327	Silver halide emulsion protein monomeric repeat unit #5.	192	1.60E-17
EF054-2	W32520	Collagen-like polypeptide SEQ ID NO:3.	189	2.40E-17
EF054-2	W32532	Collagen-like polypeptide SEQ ID NO:15.	189	2.40E-17
EF054-2	W12325	Silver halide emulsion protein monomeric repeat unit #3.	189	2.40E-17
EF054-2	W12337	Silver halide emulsion protein monomeric repeat unit #15.	189	2.40E-17
EF054-2	W12341	Silver halide emulsion FLAG(RTM)-tagged protein #2.	189	2.60E-17
EF054-2	W02098	S. mutans antigen I/II.	161	5.40E-15
EF054-2	W02096	S. mutans antigen I/II fragment (aa803-1113).	161	1.60E-13
EF059-2	R26042	P. yoelii SSP2 antigen.	344	1.90E-39
EF059-2	R85782	Group B Streptococcal mutant beta antigen without IgA binding domain.	232	1.10E-26
EF059-2	R85781	Group B Streptococcal wild-type beta antigen.	232	1.70E-26
EF059-2	P91941	Sequence of preprospasmolysin.	200	1.50E-18
EF059-2	R28150	Sugar beet chitinase 1.	148	1.70E-11

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF059-2	R26842	Protease from <i>S. Aureus</i> ATCC12600.	147	2.10E-11
EF059-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	151	2.10E-11
EF059-2	W07539	Collagen like protein (CLP).	146	3.00E-11
EF061-2	R26042	<i>P. yoelii</i> SSP2 antigen.	241	1.70E-25
EF061-2	P60570	Sequence of the Falciparum Interspersed Repeat Antigen	199	1.60E-18
EF061-2	R85782	Group B Streptococcal mutant beta antigen without IgA binding domain.	153	2.40E-14
EF061-2	R85781	Group B Streptococcal wild-type beta antigen.	153	3.60E-14
EF061-2	P91941	Sequence of preprospasmolysin.	163	9.70E-14
EF061-2	P83194	Sequence of a bioadhesive precursor protein encoded by cDNA clone	156	7.90E-13
EF061-2	R28150	Sugar beet chitinase I.	156	9.10E-13
EF061-2	W02096	<i>S. mutans</i> antigen I/II fragment (aa803-1114).	148	1.20E-12
EF061-2	P82971	Bioadhesive precursor protein from cDNA 52.	148	9.70E-12
EF061-2	W02098	<i>S. mutans</i> antigen I/II.	148	1.50E-11
EF062-2	W02098	<i>S. mutans</i> antigen I/II.	107	1.20E-36
EF062-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	132	3.00E-36
EF062-2	W02098	<i>S. mutans</i> antigen I/II	147	1.50E-11
EF062-2	W02098	<i>S. mutans</i> antigen I/II	148	9.70E-12
EF071-2	W02098	<i>S. mutans</i> antigen I/II	148	1.50E-11
EF071-2	R91515	Listeria phage lysin PL Y511	273	4.70E-37

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF075-2	W14070	S.thermophilus exopolysaccharide biosynthesis protein EpsR.	239	4.20E-36
EF075-2	W22169	S.thermophilus exopolysaccharide synthesis operon epsA gene product.	239	4.00E-34
EF077-2	R07280	Helicobacter-specific ATPase 439.	258	4.10E-74
EF077-2	R48036	Mycobacterium BCG immunogen	105	2.90E-67
EF077-2	W06712	Helicobacter-specific ATPase 948 (ORF-4).	220	2.50E-67
EF077-2	R70119	Rat homologue of human Wilson disease gene ATP7B.	186	9.80E-54
EF077-2	R72343	Wilson disease protein ATP7B.	176	6.70E-40
EF077-2	R06376	Product of the sse1 gene.	166	3.10E-28
EF077-2	R75396	Flea sodium pump alpha subunit	146	2.10E-25
EF077-2	W20891	H. pylori transporter protein, 14ce20219orf1.	156	8.60E-14
EF078-2	R56667	Bacteroides fragilis PprX regulatory response protein.	148	8.30E-18
EF078-2	R74630	Tomato TGE/ETI ethylene response protein.	130	7.80E-13
EF078-2	R69849	Ethylene response (ETR) gene product.	128	1.70E-11
EF078-2	R69850	Ethylene response (ETR) mutant protein etr1-1.	128	1.70E-11
EF078-2	R69851	Ethylene response (ETR) mutant protein etr1-2.	128	1.70E-11
EF078-2	R69852	Ethylene response (ETR) mutant protein etr1-3.	128	1.70E-11
EF081-2	R27258	Penicillin binding protein derivative #2.	101	6.20E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF081-2	R27259	Penicillin binding protein derivative #3.	101	6.20E-15
EF081-2	R27260	Penicillin binding protein derivative #4.	101	6.20E-15
EF081-2	R27261	Penicillin binding protein derivative #5.	101	6.20E-15
EF081-2	R27263	Penicillin binding protein derivative #7.	101	6.20E-15
EF081-2	R27264	Penicillin binding protein derivative #8.	101	6.20E-15
EF081-2	R27262	Penicillin binding protein derivative #6.	101	6.50E-15
EF081-2	R30845	Sequence encoded by the mec A gene.	101	6.90E-15
EF081-2	R27255	Penicillin binding protein PBP2A-27R.	101	6.90E-15
EF081-2	R31216	Penicillin binding protein PBP2A-27R.	101	7.00E-15
EF110-2	R91042	V8 mature protease (aal-213).	106	6.60E-16
EF110-2	R91043	V8 mature protease (aal-214).	106	7.20E-16
EF110-2	R91044	V8 mature protease (aal-215).	106	7.80E-16
EF110-2	R26842	Protease from <i>S. Aureus</i> ATCC12600.	106	6.70E-15
EF110-2	R29644	Protease from <i>S. Aureus</i> .	106	1.20E-14
EF110-2	W22218	Protein encoded by pV8RPT(-) construct.	106	7.60E-14
EF110-2	R91033	Beta-galactosidase-V8 protease fusion protein.	106	7.60E-14
EF110-2	R91034	Beta-galactosidase-V8 protease fusion protein.	106	1.70E-13
EF122-2	R11129	Protein encoded by pUC ES (DSM 2582).	372	1.70E-13
EF131-2	R37495	Pneumococcal fibrial protein A.	1185	6.80E-165

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF131-2	W26367	Staphylococcus aureus saliva binding protein.	418	3.70E-85
EF131-2	R79722	ROM precursor TROMP1.	171	9.00E-31
EF131-2	W22134	Treponema pallidum rare outer membrane protein (TROMP-1).	171	9.00E-31

TABLE 3. Conservative Amino Acid Substitutions.

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

Table 4. Residues comprising Antigenic Epitope-Bearing Portion

EF001-2	from about Asp-151 to about Lys-152, from about Asp-258 to about Lys-363, from about Asp-408 to about Tyr-418.	from about Tyr-418 to about Asp-258
EF002-2	from about Asp-80 to about Asp-83, from about Asp-283 to about Asp-286.	from about Gly-363 to about Asp-283
EF003-2	from about Asp-263 to about Gly-266.	from about Asp-286 to about Asp-263
EF004-2	from about Asn-23 to about Asn-26, from about Thr-154 to about Asp-159.	from about Ser-87, Thr-154 to about Asp-159
EF005-2	from about Lys-249 to about Glu-252.	from about Asp-159 to about Lys-249
EF006-2	from about Gly-23 to about Asp-28.	from about Asp-28 to about Gly-23
EF008-2	from about Thr-92 to about Gly-94, from about Thr-165 to about Gly-287 to about Thr-289.	from about Asp-287 to about Thr-92
EF010-2	from about Pro-129 to about Asn-131.	from about Asp-289 to about Pro-129
EF012-2	from about Asp-77 to about Asp-79, from about Thr-256 to about Thr-258, from about Asp-468 to about Thr-256.	from about Lys-98, Thr-256 to about Asp-77
EF013-2	from about Thr-30 to about Asp-32, from about Thr-164 to about Asn-166, from about Thr-195 to about Thr-198.	from about Ala-75, Thr-195 to about Gly-316
EF014-2	from about Ser-203 to about Asp-206, from about Thr-316 to about Thr-319.	from about Gly-316 to about Ser-203
EF015-2	from about Pro-66 to about Gly-69.	from about Asp-206 to about Pro-66
EF016-2	from about Lys-236 to about Asn-239.	from about Asp-239 to about Lys-236
EF017-2	from about Ser-90 to about Gly-93, from about Thr-199 to about Lys-230 to about Asn-233, from about Gly-431 to about Thr-434.	from about Lys-230 to about Ser-90
EF018-2	from about Lys-159 to about Tyr-161, from about Thr-167 to about Asn-250 to about Arg-256, from about Gly-395 to about Lys-416 to about Tyr-418.	from about Ser-42 to about Thr-167 to about Tyr-418

Table 4. Residues Comprising Antigenic Epitope-Bearing Port

	about Arg-430.	
EF019-2	from about Arg-209 to about Ser-211, from abo 290.	about Ser-
EF020-2	from about Lys-57 to about Asn-62.	
EF021-2	from about Ser-33 to about Gly-35, from about from about Asp-139 to about Lys-141, from abo 258, from about Gln-271 to about Tyr-277.	at Gly-81, about Ser-
EF023-2	from about Lys-232 to about Asp-234, from abo 306, from about Thr-453 to about Arg-456, from Thr-480.	about Gly- 8 to about
EF025-2	from about Arg-183 to about Asp-185.	
EF026-2	from about Ser-25 to about Asp-30, from about from about Gln-107 to about Asn-110.	out Asp-94,
EF027-2	from about Gln-72 to about Lys-74, from about 231.	out Asp-
EF028-2	from about Asp-186 to about Gln-188.	
EF029-2	from about Asp-118 to about Lys-122, from abo Tyr-126.	to about
EF031-2	from about Glu-30 to about Gly-33.	
EF034-2	from about Glu-25 to about Gly-27, from about	out Thr-77.
EF36-2	from about Gln-177 to about Ser-179.	
EF037-2	from about Ser-25 to about Asp-30, from about from about Gln-107 to about Asn-110.	out Asp-94,
EF038-2	from about Asn-77 to about Lys-79, from about	out Asn-92.
EF040-2	from about Lys-167 to about Gly-172, from abo Asn-242.	about

Table 4. Residues comprising Antigenic Epitope-Bearing Portion

EF044-2	from about Asp-162 to about Gly-194, from about 2	about Asn-
EF045-2	from about Asp-158 to about Asn-161, from about 174, from about Tyr-261 to about Gly-264, from Gly-338.	about Gly-264 to about
EF046-2	from about Ser-18 to about Gly-23, from about from about Thr-76 to about Asp-78.	Ser-47,
EF047-2	from about Asn-28 to about Asp-30, from about 277.	about Asn-
EF048-2	from about Asp-138 to about Lys-141, from about Gly-154.	about
EF051-2	from about Asp-73 to about Gly-76	
EF053-2	from about Ser-79 to about Gly-82.	
EF055-2	from about Asp-26 to about Gly-28, from about from about Arg-71 to about Gly-74, from about	about Asp-69, about Gly-89.
EF056-2	from about Arg-71 to about Gly-74, from about	about Gly-89.
EF058-2	from about Lys-129 to about Gly-133, from about 573, from about Pro-586 to about Gly-591.	about Tyr-
EF065-2	from about Ser-236 to about Tyr-239, from about 352, from about Lys-415 to about Asn-418, from about Asp-448, from about Asn-489 to about Lys-491, about Asp-518, from about Glu-639 to about L	about Gly-46 to about Ser-516 to
EF066-2	from about Ser-236 to about Tyr-239, from about 352, from about Lys-415 to about Asn-418, from about Asp-448, from about Asn-489 to about Lys-491, about Asp-518, from about Glu-639 to about L	about Gly-46 to about Ser-516 to
EF067-2	from about Ser-236 to about Tyr-239, from about 352, from about Lys-415 to about Asn-418, from about Asp-448, from about Asn-489 to about Lys-491, about Asp-518, from about Glu-639 to about L	about Gly-46 to about Ser-516 to

Table 4. Residues Comprising Antigenic Epitope-Bearing Porti

EF073-2	from about Met-98 to about Arg-100, from abo 112	about Asp-
EF074-2	from about Ser-53 to about Tyr-59, from about from about Pro-97 to about Gln-100, from abou 232.	about Gly-88, about Gly-
EF076-2	from about Asn-38 to about Tyr-40, from abou from about Lys-79 to about Gly-81.	about Asn-53,
EF077-2	from about Arg-411 to about Gly-413.	
EF078-2	from about Thr-294 to about Gly-296, from abo 368, from about Glu-524 to about Gly-526.	about Gln-
EF080-2	from about Glu-164 to about Gly-166, from abo 208, from about Lys-239 to about Gly-243.	about Tyr-
EF081-2	from about Asn-7 to about Ser-11, from about from about Lys-112 to about Asn-114, from ab 164, from about Arg-181 to about Gly-183.	about Tyr-80, about Asp-
EF083-2	from about Gln-38 to about Arg-40.	
EF084-2	from about Lys-140 to about Asp-142, from ab 166, from about Arg-262 to about Gly-264	about Arg-
EF085-2	from about Asn-95 to about Asp-97, from about 114, from about Asp-258 to about Ser-260, from Ser-403.	about Asp- to about
EF086-2	from about Pro-112 to about Gly-115, from abo 224, from about Asn-296 to about Gly-299, fro Lys-348, from about Asp-428 to about Ser-432	about Ser- to about
EF087-2	from about Pro-112 to about Gly-115, from abo 224, from about Asn-296 to about Gly-299, fro Lys-348, from about Asp-428 to about Ser-432	about Ser- to about
EF088-2	from about Pro-112 to about Gly-115, from abo 224, from about Asn-296 to about Gly-299, fro Lys-348, from about Asp-428 to about Ser-432	about Ser- to about

Table 4. Residues comprising Antigen 2 Immune-Bearing Portion

EF090-2	from about Asp-21 to about Asp-5.	
EF091-2	from about Gln-4 to about Asp-43.	
EF093-2	from about Lys-5 to about Gln-97.	
EF094-2	from about Asp-314 to about Asp-316.	
EF095-2	from about Ser-328 to about Thr-330, from about Ser-361 to about Gln-37 to about Gly-639, from about Gly-746.	from about Asp-314 to about Asp-316.
EF096-2	from about Lys-128 to about Asn-130, from about Lys-190 to about Asp-192.	from about Asp-314 to about Asp-316.
EF097-2	from about Val-357 to about Gly-359.	
EF099-2	from about Gln-44 to about Asp-47, from about Lys-150 to about Asn-286 to about Asp-289.	from about Gly-637 to about Gly-639.
EF101-2	from about Lys-40 to about Asp-42, from about Lys-253 to about Lys-288 to about Gly-290.	from about Asn-286 to about Asn-288.
EF102-2	from about Asp-314 to about Asp-316.	
EF103-2	from about Asn-46 to about Gly-48.	
EF104-2	from about Pro-232 to about Lys-237, from about Ser-361 to about Ser-421 to about Gly-423, from about Ser-490, from about Asp-550 to about Asn-552 to about Lys-640, from about Asp-727 to about Gln-751 to about Ser-754, from about Lys-771 to about Ile-835 to about Asn-837, from about Pro-851 to about Asp-853.	from about Asn-550 to about Asn-552 to about Gly-637 to about Asn-639 to about Lys-640 to about Lys-642 to about Lys-644 to about Lys-646 to about Lys-648 to about Lys-650 to about Lys-652 to about Lys-654 to about Lys-656 to about Lys-658 to about Lys-660 to about Lys-662 to about Lys-664 to about Lys-666 to about Lys-668 to about Lys-670 to about Lys-672 to about Lys-674 to about Lys-676 to about Lys-678 to about Lys-680 to about Lys-682 to about Lys-684 to about Lys-686 to about Lys-688 to about Lys-690 to about Lys-692 to about Lys-694 to about Lys-696 to about Lys-698 to about Lys-700 to about Lys-702 to about Lys-704 to about Lys-706 to about Lys-708 to about Lys-710 to about Lys-712 to about Lys-714 to about Lys-716 to about Lys-718 to about Lys-720 to about Lys-722 to about Lys-724 to about Lys-726 to about Lys-728 to about Lys-730 to about Lys-732 to about Lys-734 to about Lys-736 to about Lys-738 to about Lys-740 to about Lys-742 to about Lys-744 to about Lys-746 to about Lys-748 to about Lys-750 to about Lys-752 to about Lys-754 to about Lys-756 to about Lys-758 to about Lys-760 to about Lys-762 to about Lys-764 to about Lys-766 to about Lys-768 to about Lys-770 to about Lys-772 to about Lys-774 to about Lys-776 to about Lys-778 to about Lys-780 to about Lys-782 to about Lys-784 to about Lys-786 to about Lys-788 to about Lys-790 to about Lys-792 to about Lys-794 to about Lys-796 to about Lys-798 to about Lys-800 to about Lys-802 to about Lys-804 to about Lys-806 to about Lys-808 to about Lys-810 to about Lys-812 to about Lys-814 to about Lys-816 to about Lys-818 to about Lys-820 to about Lys-822 to about Lys-824 to about Lys-826 to about Lys-828 to about Lys-830 to about Lys-832 to about Lys-834 to about Lys-836 to about Lys-838 to about Lys-840 to about Lys-842 to about Lys-844 to about Lys-846 to about Lys-848 to about Lys-850 to about Lys-852 to about Lys-854 to about Lys-856 to about Lys-858 to about Lys-860 to about Lys-862 to about Lys-864 to about Lys-866 to about Lys-868 to about Lys-870 to about Lys-872 to about Lys-874 to about Lys-876 to about Lys-878 to about Lys-880 to about Lys-882 to about Lys-884 to about Lys-886 to about Lys-888 to about Lys-890 to about Lys-892 to about Lys-894 to about Lys-896 to about Lys-898 to about Lys-900 to about Lys-902 to about Lys-904 to about Lys-906 to about Lys-908 to about Lys-910 to about Lys-912 to about Lys-914 to about Lys-916 to about Lys-918 to about Lys-920 to about Lys-922 to about Lys-924 to about Lys-926 to about Lys-928 to about Lys-930 to about Lys-932 to about Lys-934 to about Lys-936 to about Lys-938 to about Lys-940 to about Lys-942 to about Lys-944 to about Lys-946 to about Lys-948 to about Lys-950 to about Lys-952 to about Lys-954 to about Lys-956 to about Lys-958 to about Lys-960 to about Lys-962 to about Lys-964 to about Lys-966 to about Lys-968 to about Lys-970 to about Lys-972 to about Lys-974 to about Lys-976 to about Lys-978 to about Lys-980 to about Lys-982 to about Lys-984 to about Lys-986 to about Lys-988 to about Lys-990 to about Lys-992 to about Lys-994 to about Lys-996 to about Lys-998.
EF105-2	from about Ser-40 to about Gly-43, from about Lys-253 to about Lys-288 to about Gly-290, from about Gln-220 to about Gly-222, from about Lys-265 to about Lys-267.	from about Gln-97, from about Gly-637 to about Gly-639.
EF106-2	from about Asp-72 to about Gly-75, from about Lys-277 to about Asn-310 to about Arg-313.	from about Asp-314 to about Asp-316.
EF107-2	from about Lys-155 to about Asn-157, from about Lys-159 to about Asn-161.	from about Asp-314 to about Asp-316.

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion

	191, from about Arg-270 to about Gly-272, from Lys-335, from about Asp-365 to about Asp-369, about Asp-422, from about Gly-485 to about Thr-487.	from about Thr-451 to about Thr-453.
EF108-2	from about Lys-142 to about Trp-145, from about Thr-150, from about Arg-212 to about Gly-214, from about Asp-251, from about Asp-384 to about Asp-387, about Arg-485, from about Lys-491 to about Gly-493, from about Gly-619 to about Gly-624, from about Asp-656 to about Lys-717 to about Asn-721, from about Ser-822 to about Tyr-1137 to about Thr-1141.	from about Tyr-1141 to about Thr-1143, from about Thr-1481 to about Thr-1483, from about Thr-1485 to about Thr-1487.
EF110-2	from about Pro-123 to about Gly-127, from about Thr-225.	from about Gly-127 to about Thr-225.
EF111-2	from about Lys-207 to about Asn-209, from about Asn-248, from about Lys-396 to about Asp-398, from about Ser-432, from about Thr-470 to about Thr-472.	from about Thr-429 to about Thr-431.
EF119-2	from about Asp-90 to about Asn-92, from about Thr-143.	from about Gly-143 to about Thr-145.
EF121-2	from about Asn-159 to about Asp-161, from about Lys-353, from about Pro-658 to about Gly-660, from about Ser-789.	from about Asn-786 to about Thr-788.
EF122-2	from about Asn-159 to about Asp-161, from about Lys-353, from about Pro-658 to about Gly-660, from about Ser-789.	from about Asn-786 to about Thr-788.
EF123-2	from about Asn-331 to about Arg-336, from about Thr-636, from about Glu-780 to about Ser-782, from about Asn-911, from about Lys-939 to about Glu-942, about Gly-1076, from about Asp-1367 to about Pro-1433 to about Lys-1435, from about Gly-1437 to about Lys-1656 to about Asp-1660, from about Glu-1863, from about Ser-1916 to about Gln-1918 to about Gly-1942.	from about Gly-1942 to about Thr-1944, from about Asp-1074 to about Thr-1518, from about Thr-1518 to about Pro-1940.
EF124-2	from about Asn-331 to about Arg-336, from about Thr-636, from about Glu-780 to about Ser-782, from about Asn-911, from about Lys-939 to about Glu-942, about Gly-1076, from about Asp-1367 to about Pro-1433 to about Lys-1435, from about Gly-1437 to about Lys-1656 to about Asp-1660, from about Glu-1863, from about Ser-1916 to about Gln-1918 to about Gly-1942.	from about Gly-1942 to about Thr-1944, from about Asp-1074 to about Thr-1518, from about Thr-1518 to about Pro-1940.

INDICATIONS RELATING TO A DEPOSITED

ANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>10</u> , line <u>12</u>		
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What Is Claimed:

1. An isolated nucleic acid molecule comprising a polynucleotide sequence selected from a group consisting of:
 - (a) a nucleotide sequence encoding any one of the amino acid polypeptides shown in Table 1; or
 - (b) a nucleotide sequence complementary to any one of the sequences in (a);
 - (c) a nucleotide sequence at least 95% identical to any one of the sequences shown in Table 1; or
 - (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences shown in Table 1.
2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide sequence identical to a nucleotide sequence in (a) or (c).
3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) or (b).
4. The isolated nucleic acid molecule of claim 3, wherein the epitope-bearing portion of a polypeptide comprises an amino acid sequence listed in Table 1.
5. A method for making a recombinant vector comprising inserting a nucleic acid molecule of claim 1 into a vector.
6. A recombinant vector produced by the method of claim 5.
7. A host cell comprising the vector of claim 6.
8. A method of producing a polypeptide comprising:
 - (a) growing the host cell of claim 7 such that the protein is expressed in the host cell; and
 - (b) recovering the expressed polypeptide.
9. An isolated polypeptide comprising a polypeptide selected from a group consisting of:
 - (a) a polypeptide consisting of one of the complete amino acid sequences of Table 1;
 - (b) a polypeptide consisting of one the complete amino acid sequence of Table 1 except the N-terminal residue.

- (c) a fragment of the polypeptide of (a) having biological activity, and
- (d) a fragment of the polypeptide of (a) which binds to an antibody specific for the polypeptide of (a).
10. An isolated antibody specific for the polypeptide of claim 9.
11. A polypeptide produced according to the method of claim 9.
12. An isolated polypeptide comprising an amino acid sequence which is identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.
13. An isolated polypeptide antigen comprising an amino acid sequence which is identical to an *E. faecalis* epitope shown in Table 4.
14. An isolated nucleic acid molecule comprising a polynucleotide sequence encoding a polypeptide of claim 9.
15. A hybridoma which produces an antibody of claim 10.
16. A vaccine, comprising:
- (1) one or more *E. faecalis* polypeptides selected from the group consisting of a polypeptide of claim 9; and
 - (2) a pharmaceutically acceptable diluent, carrier, or excipient, wherein said polypeptide is present, in an amount effective to elicit the production of antibodies in an animal to a member of the *Enterococcus* genus.
17. A method of preventing or attenuating an infection caused by a member of the *Enterococcus* genus in an animal, comprising administering to the animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.
18. A method of detecting *Enterococcus* nucleic acids in a biological sample, comprising:
- (a) contacting the sample with one or more nucleic acids under conditions such that hybridization occurs, and
 - (b) detecting hybridization of said nucleic acids to the one or more nucleic acid sequences present in the biological sample.

19. A method of detecting *Leptospira* nucleic acids in a sample obtained from an animal, comprising:
- (a) amplifying one or more *Leptospira* nucleic acids in the sample using polymerase chain reaction;
 - (b) detecting said amplified *Leptospira* nucleic acids.
20. A kit for detecting *Leptospira* antibodies in a blood sample obtained from an animal, comprising:
- (a) a polypeptide of claim 1 attached to a solid support;
 - (b) detecting means.
21. A method of detecting *Leptospira* antibodies in a sample obtained from an animal, comprising:
- (a) contacting the sample with a polypeptide of claim 9;
 - (b) detecting antibody-antigen complexes.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT

TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68, C12N 1/21, 5/12, G01N 33/569, 33/68, A61K 39/09		(11) International Publication Number: A3	WO 98/50554	
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(22) International Filing Date: 4 May 1998 (04.05.98)		(81) Designated States: BY, CA, CH, CN, DE, DK, EE, ES, FI, GB, GE, GR, HK, IG, JP, KR, KZ, LC, LK, LR, LU, LV, MA, MG, MK, MN, MW, MX, NO, NZ, OM, PA, PE, PG, PH, PL, PT, RU, SC, SE, SG, SI, SK, SL, SN, SV, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO (GH, GM, KE, LS, SD, SL, SZ, TZ, UG, ZW), Eurasian (AM, AZ, BY, GE, GZ, IL, IN, JP, KG, MD, RU, TJ, TM), European (AT, BE, BF, BG, BR, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, SL, SN, TD, TG).		
(30) Priority Data: 60/044,031 6 May 1997 (06.05.97) US 60/046,655 16 May 1997 (16.05.97) US 60/066,009 14 November 1997 (14.11.97) US		(88) Date of publication: 1 April 1999 (01.04.99)		
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(74) Agents: BROOKES, A., Anders et al; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).				
(54) Title: <i>ENTEROCOCCUS FAECALIS</i> POLYNUCLEOTIDES AND POLYPEPTIDES				
(57) Abstract <p>The present invention relates to novel genes from <i>Enterococcus faecalis</i> and the polynucleotide vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to <i>Enterococcus</i> nucleic acids, polypeptides and antibodies in a biological sample. The present invention also relates to the prevention or attenuation of infection by <i>Enterococcus</i>.</p>				

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INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 6 C12N15/31 C07K14/31 C07K16/12 C12Q1/68
 C12N5/12 G01N33/58 G01N33/68 A61K39/09

According to International Patent Classification (IPC) or to international classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 6 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included

Electronic data base consulted during the international search (name of data base and, where practical, search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category * Citation of document, with indication, where appropriate, of the relevant passages

A EVERS S & COURVALIN R: "Regulation of VanB-Type vancomycin resistance gene expression by the VanS(E)-VanR (B) two-component regulatory system in Enterococcus faecalis 9583." JOURNAL OF BACTERIOLOGY, vol. 178, 1996, pages 1302-1309, XP000073904 see abstract

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☒ Further documents are listed in the continuation of box C

☒ Patent family members

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
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X document of particular interest which cannot be considered to involve an inventive step

Y document of particular interest which cannot be considered to involve an inventive step when the document is combined with other documents, such combinations in the art.

Z document member of a

Date of the actual completion of the international search

2 September 1998

Date of mailing of the

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INTERNATIONAL SEARCH REPORT

C.(Continuation) DOCUMENTS REFERRED TO BY CLAIMANT		
Category *	Citation of document, its publication, where available, and relevant passages	Page No.
A	CLARK I M ET AL: "ISOLATION AND SEQUENCE DETERMINATION OF AN ENDODOMINANT ANTIGEN FROM ENTEROCOCCUS FAECALIS" SERODIAGNOSIS AND IMMUNOTHERAPY IN INFECTIOUS DISEASE, vol. 5, no. 2, July 1993, pages 85-92, XP00203536 see abstract see figure 3	21
A	LOWE A M ET AL: "Cloning of an Enterococcus faecalis endocarditis antigen: homology with adhesins from some oral Streptococci." INFECTION AND IMMUNITY, vol. 63, no. 2, February 1995, pages 703-706, XP00203905 see abstract see figure 2	21
A	BURNIE J P & CLARK I M: "Diagnosing endocarditis with the cloned 112 kDa antigen of Enterococcus faecalis." JOURNAL OF IMMUNOLOGICAL METHODS, vol. 123, 1989, pages 217-225, XP00074342 see abstract see page 222, column 1, paragraph 2	201
P,A	XU Y ET AL: "Enterococcus faecalis antigens in human infections." INFECTION AND IMMUNITY, vol. 65, no. 10, October 1997, pages 4207-4215, XP00073906 see abstract	201
X	EP 0 652 291 A (FUSO PHARMACEUTICAL IND ;OHNO TSUNEYA (JP)) 12 May 1995 see abstract see page 4, line 27 - line 31 see claim 5	19

INTERNATIONAL SEARCH REPORT

Box I Observations where certain claims were found unsearchable (Continuation of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17 of the Patent Cooperation Treaty.

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim(s) 17
is(are) directed to a method of treatment of
body, the search has been carried out and the
effects of the compound/composition.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the
an extent that no meaningful international search can be carried out, specifically:
Further defects(s) under article 17(2)(a):
The gene EF07E which is mentioned in Table 4, is not
and is also absent from the sequence listing.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second

sheet)

ving reasons.

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file 1

Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 5)

This International Searching Authority found multiple inventions in this International application.

1. ☐ As all required additional search fees were timely paid by the applicant, this International search is restricted to the invention first mentioned in the claims, namely claims Nos. 1-17.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, the search is not restricted to the invention first mentioned in the claims, namely claims Nos. 1-17.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, the search is restricted to the invention first mentioned in the claims, namely claims Nos. 1-17.
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, the search is restricted to the invention first mentioned in the claims, namely claims Nos. 1-17.

See extra sheet, Invention 1.

Remark on Protest

- ☐ The additional search fees were
☐ No protest accompanied the payment of the additional search fees.

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re payment

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applicant's protest.

in fees.

FURTHER INFORMATION CONTINUED FROM PCT No. 210

Inventions 7 to 41: Claims: (1-3) partially

Idem as invention 1, but concerning EF008 to

Inventions 42 to 74: Claims: (1-3) partially

Idem as invention 1, but concerning EF046 to

Inventions 75 to 107: Claims: (1-3) partially

Idem as invention 1, but concerning EF079 to

Inventions 108 to 123: Claims: (1-3) partially

Idem as invention 1, but concerning EF117 to

Invention 124: Claim: 11 partially

An isolated polypeptide antigen comprising an
sequence of an *Enterobacter faecalis* epitope
Table 4.

For the sake of conciseness, the first subject matter
defined, the other subject matters are defined by a

INTERNATIONAL SEARCH REPORT

Information on patent family members

Inter-
PC

Patent document cited in search report	Publication date	Patent family member(s)	Priority date
EP 0652291 A	10-08-85	AU 684250 E	87
		AU 4513593 A	84
		US 5807673 A	88
		WO 9401583 A	84
		JP 2798499 E	88
		US 5763188 A	88
		US 5770375 A	88
		US 5798211 A	88

